

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Beavo, Joseph A.
Bentley, Kelley
Charbonneau, Harry
Sonnenburg, William K.
- (ii) TITLE OF INVENTION: DNA Encoding Mammalian
Phosphodiesterases
- (iii) NUMBER OF SEQUENCES: 58
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
Bicknell
 - (B) STREET: Two First National Plaza, 20 South Clark
Street
 - (C) CITY: Chicago
 - (D) STATE: Illinois
 - (E) COUNTRY: USA
 - (F) ZIP: 60603
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 07/688,356
 - (B) FILING DATE: 04-APR-1991
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Noland, Greta E.
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 - (C) REFERENCE/DOCKET NUMBER: 27866/30822
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (312) 346-5750
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 - (C) TELEX: 25-3856

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AARATGGGNA TGAARAARAA

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Lys Met Gly Met Met Lys Lys Lys
1 5

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ACRTTCATYT CYTCYTCYTG CAT

23

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4

Met Gln Glu Glu Glu Met Asn Val
1 5

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2291 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 100..1689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGCTCAGAAA CTGTAGGAAT TCTGATGTGC TTCGGTGCAT GGAACAGTAA CAGATGAGCT	60
GCTTTGGGGA GAGCTGGAAC GCTCAGTCGG AGTATCATC ATG GGG TCT ACT GCT	114
Met Gly Ser Thr Ala	5
1	
ACA GAA ACT GAA GAA CTG GAA AAC ACT ACT TTT AAG TAT CTC ATT GGA	162
Thr Glu Thr Glu Leu Glu Asn Thr Thr Phe Lys Tyr Leu Ile Gly	20
10	
15	
GAA CAG ACT GAA AAA ATG TGG CAA CGC CTG AAA GGA ATA CTA AGA TGC	210
Glu Gln Thr Lys Met Trp Gln Arg Leu Lys Gly Ile Leu Arg Cys	35
25	
30	
TTA GTG AAG CAG CTG GAA AAA GGT GAT GTT AAC GTC ATC GAC TTA AAG	258
Leu Val Lys Gln Leu Glu Lys Gly Asp Val Asn Val Ile Asp Leu Lys	50
40	
45	
AAG AAT ATT GAA TAT GCA GCA TCT GTG TTG GAA GCA GTT TAT ATT GAT	306
Lys Asn Ile Glu Tyr Ala Ala Ser Val Leu Glu Ala Val Tyr Ile Asp	65
55	
60	
GAA ACA AGG AGA CTG CTG GAC ACC GAT GAT GAG CTC AGT GAC ATT CAG	354
Glu Thr Arg Arg Leu Leu Asp Thr Asp Asp Glu Leu Ser Asp Ile Gln	85
70	
75	
80	
TGG GAT TCC GTC CCA TCA GAA GTC CGG GAC TGG TTG GCT TCT ACC TTT	402
Ser Asp Ser Val Pro Ser Glu Val Arg Asp Trp Leu Ala Ser Thr Phe	100
90	
95	
ACA CGG AAA ATG GGG ATG ATG AAA AAG AAA TCT GAG GAA AAA CCA AGA	450
Thr Arg Lys Met Gly Met Met Lys Lys Lys Ser Glu Glu Lys Pro Arg	115
105	
110	
TTT CGG AGC ATT GTG CAT GTT GTT CAA GCT GGA ATT TTT GTG GAA AGA	498
Phe Arg Ser Ile Val His Val Val Gln Ala Gly Ile Phe Val Glu Arg	130
120	
125	
130	
ATG TAC AGA AAG TCC TAT CAC ATG GTT GGC TTG GCA TAT CCA GAG GCT	546
Met Tyr Arg Lys Ser Tyr His Met Val Gly Leu Ala Tyr Pro Glu Ala	145
135	
140	
145	
GTC ATA GTA ACA TTA AAG GAT GTT GAT AAA TGG TCT TTT GAT GTA TTT	594
Val Ile Val Thr Leu Lys Asp Val Asp Lys Trp Ser Phe Asp Val Phe	165
150	
155	
160	
GCC TTG AAT GAA GCA AGT GGA GAA CAC AGT CTG AAG TTT ATG ATT TAT	642
Ala Leu Asn Glu Ala Ser Gly Glu His Ser Leu Lys Phe Met Ile Tyr	180
170	
175	
GAA CTA TTC ACC AGA TAT GAT CTT ATC AAC CGT TTC AAG ATT CCT GTT	690
Glu Leu Phe Thr Arg Tyr Asp Leu Ile Asn Arg Phe Lys Ile Pro Val	195
185	
190	
TCT TGC CTA ATT GCC TTT GCA GAA GCT CTA GAA GTT GGT TAC AGC AAG	738
Ser Cys Leu Ile Ala Phe Ala Glu Ala Leu Glu Val Gly Tyr Ser Lys	210
200	
205	
210	
TAC AAA AAT CCA TAC CAC AAT TTG ATT CAT GCA GCT GAT GTC ACT CAA	786
Tyr Lys Asn Pro Tyr His Asn Leu Ile His Ala Ala Asp Val Thr Gln	225
215	
220	
225	
ACT GTG CAT TAC ATA ATG CTT CAT ACA GGT ATC ATG CAC TGG CTC ACT	834
Thr Val His Tyr Ile Met Leu His Thr Gly Ile Met His Trp Leu Thr	245
230	
235	
240	
245	

GAA CTG GAA ATT TTA GCA ATG GTC TTT GCC GCT GCC ATT CAT GAC TAT Glu Leu Glu Ile Leu Ala Met Val Phe Ala Ala Ala Ile His Asp Tyr 250 255 260	882
GAG CAT ACA GGG ACT ACA AAC AAT TTT CAC ATT CAG ACA AGG TCA GAT Glu His Thr Gly Thr Thr Asn Asn Phe His Ile Gln Thr Arg Ser Asp 265 270 275	930
GTT GCC ATT TTG TAT AAT GAT CGC TCT GTC CTT GAA AAT CAT CAT GTG Val Ala Ile Leu Tyr Asn Asp Arg Ser Val Leu Glu Asn His His Val 280 285 290	978
AGT GCA GCT TAT CGC CTT ATG CAA GAA GAA GAA ATG AAT GTC CTG ATA Ser Ala Ala Tyr Arg Leu Met Gln Glu Glu Glu Met Asn Val Leu Ile 295 300 305	1026
AAT TTA TCC AAA GAT GAC TGG AGG GAT CTT CGG AAC CTA GTG ATT GAA Asn Leu Ser Lys Asp Asp Trp Arg Asp Leu Arg Asn Leu Val Ile Glu 310 315 320 325	1074
ATG GTG TTG TCT ACA GAC ATG TCG GGT CAC TTC CAG CAA ATT AAA AAT Met Val Leu Ser Thr Asp Met Ser Gly His Phe Gln Gln Ile Lys Asn 330 335 340	1122
ATA AGA AAT AGT TTG CAG CAA CCT GAA GGG CTT GAC AAA GCC AAA ACC Ile Arg Asn Ser Leu Gln Gln Pro Glu Gly Leu Asp Lys Ala Lys Thr 345 350 355	1170
ATG TCC CTG ATT CTC CAT GCA GCA GAC ATC AGT CAC CCA GCC AAA TCC Met Ser Leu Ile Leu His Ala Ala Asp Ile Ser His Pro Ala Lys Ser 360 365 370	1218
TGG AAG CTG CAC CAC CGA TGG ACC ATG GCC CTA ATG GAG GAG TTT TTC Trp Lys Leu His His Arg Trp Thr Met Ala Leu Met Glu Glu Phe Phe 375 380 385	1266
CTA CAG GGA GAT AAA GAA GCT GAA TTA GGG CTT CCA TTT TCC CCG CTT Leu Gln Gly Asp Lys Glu Ala Glu Leu Gly Leu Pro Phe Ser Pro Leu 390 395 400 405	1314
TGC GAT CGG AAG TCA ACG ATG GTG GCC CAG TCC CAA ATA GGT TTC ATT Cys Asp Arg Lys Ser Thr Met Val Ala Gln Ser Gln Ile Gly Phe Ile 410 415 420	1362
GAT TTC ATA GTA GAA CCA ACA TTT TCT CTT CTG ACA GAC TCA ACA GAG Asp Phe Ile Val Glu Pro Thr Phe Ser Leu Leu Thr Asp Ser Thr Glu 425 430 435	1410
AAA ATT ATT ATT CCT CTT ATA GAG GAA GAC TCG AAA ACC AAA ACT CCT Lys Ile Ile Ile Pro Leu Ile Glu Glu Asp Ser Lys Thr Lys Thr Pro 440 445 450	1458
TCC TAT GGA GCA AGC AGA CGA TCA AAT ATG AAA GGC ACC ACC AAT GAT Ser Tyr Gly Ala Ser Arg Arg Ser Asn Met Lys Gly Thr Thr Asn Asp 455 460 465	1506
GGA ACC TAC TCC CCC GAC TAC TCC CTT GCC AGC GTG GAC CTG AAG AGC Gly Thr Tyr Ser Pro Asp Tyr Ser Leu Ala Ser Val Asp Leu Lys Ser 470 475 480 485	1554
TTC AAA AAC AGC CTG GTG GAC ATC ATC CAG CAG AAC AAA GAG AGG TGG Phe Lys Asn Ser Leu Val Asp Ile Ile Gln Gln Asn Lys Glu Arg Trp 490 495 500	1602
AAA GAG TTA GCT GCT CAA GGT GAA CCT GAT CCC CAT AAG AAC TCA GAT Lys Glu Leu Ala Ala Gln Gly Glu Pro Asp Pro His Lys Asn S r Asp 505 510 515	1650

CTA GTA AAT GCT GAA GAA AAA CAT GCT GAA ACA CAT TCA TAGGTCTGAA	1699
Leu Val Asn Ala Glu Glu Lys His Ala Glu Thr His Ser	
520 525 530	
ACACCTGAAA GACGTCTTTC ATTCTAAGGA TGGGAGGAAA CAAATTCACA AGAAATCATG	1759
AAGACATATA AAAGCTACAT ATGCATAAAA AACTCTGAAT TCAGGTCCCC ATGGCTGTCA	1819
CAAATGAATG AACAGAACTC CCAACCCCGC CTTTTTTTAA TATAATGAAA GTGCCTTAGC	1879
ATGGTTGCAG CTGTCACCAC TACAGTGTTC TACAGACGGT TTCTACTGAG CATCACAATA	1939
AAGAGAATCT TGCATTACAA AAAAAAGAAA AAAATGTGGC TCGCTTTTAA GATGAAGCAT	1999
TTCCCAGTAT TTCTGAGTCA GTTGTAAAGAT TCTTTAATCG ATACTAATAG TTTCACTAAT	2059
AGCCACTGTC AGTGTACACG ACTGTGATGA AATCTTATAC TTAGTCCTTC AACAGTTCCA	2119
GAGTTGTGAC TGTGCTTAAT AGTTTGATA TGAATTCTGG ATAGAAATCA AATCACAAC	2179
TGCATAGAAA TTTTAAAAAC CAGCTCCATA TTAAATTTTT TTAAGATATT GTCTTGATT	2239
GAAACTCCAA TACTTTGGCC ACCTGATGCA AAGAGCTGAC TCATTGAAA CC	2291

(2) INFORMATION FOR SEQ ID NO:6

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 530 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6

Met	Gly	Ser	Thr	Ala	Thr	Glu	Thr	Glu	Glu	Leu	Glu	Asn	Thr	Thr	Phe
1				5					10					15	
Lys	Tyr	Leu	Ile	Gly	Glu	Gln	Thr	Glu	Lys	Met	Trp	Gln	Arg	Leu	Lys
		20						25					30		
Gly	Ile	Leu	Arg	Cys	Leu	Val	Lys	Gln	Leu	Glu	Lys	Gly	Asp	Val	Asn
		35					40					45			
Val	Ile	Asp	Leu	Lys	Lys	Asn	Ile	Glu	Tyr	Ala	Ala	Ser	Val	Leu	Glu
		50				55					60				
Ala	Val	Tyr	Ile	Asp	Glu	Thr	Arg	Arg	Leu	Leu	Asp	Thr	Asp	Asp	Glu
		65			70					75					80
Leu	Ser	Asp	Ile	Gln	Ser	Asp	Ser	Val	Pro	Ser	Glu	Val	Arg	Asp	Trp
			85					90					95		
Leu	Ala	Ser	Thr	Phe	Thr	Arg	Lys	Met	Gly	Met	Met	Lys	Lys	Lys	Ser
			100					105					110		
Glu	Glu	Lys	Pro	Arg	Phe	Arg	Ser	Ile	Val	His	Val	Val	Gln	Ala	Gly
		115					120					125			
Ile	Phe	Val	Glu	Arg	Met	Tyr	Arg	Lys	Ser	Tyr	His	Met	Val	Gly	Leu
		130				135					140				
Ala	Tyr	Pro	Glu	Ala	Val	Ile	Val	Thr	Leu	Lys	Asp	Val	Asp	Lys	Trp
145					150					155					160

Ser	Phe	Asp	Val	Phe	Ala	Leu	Asn	Glu	Ala	Ser	Gly	Glu	His	Ser	Leu
				165					170					175	
Lys	Phe	Met	Ile	Tyr	Glu	Leu	Phe	Thr	Arg	Tyr	Asp	Leu	Ile	Asn	Arg
			180					185					190		
Phe	Lys	Ile	Pro	Val	Ser	Cys	Leu	Ile	Ala	Phe	Ala	Glu	Ala	Leu	Glu
		195					200					205			
Val	Gly	Tyr	Ser	Lys	Tyr	Lys	Asn	Pro	Tyr	His	Asn	Leu	Ile	His	Ala
	210					215					220				
Ala	Asp	Val	Thr	Gln	Thr	Val	His	Tyr	Ile	Met	Leu	His	Thr	Gly	Ile
225					230					235					240
Met	His	Trp	Leu	Thr	Glu	Leu	Glu	Ile	Leu	Ala	Met	Val	Phe	Ala	Ala
			245						250					255	
Ala	Ile	His	Asp	Tyr	Glu	His	Thr	Gly	Thr	Thr	Asn	Asn	Phe	His	Ile
			260					265						270	
Gln	Thr	Arg	Ser	Asp	Val	Ala	Ile	Leu	Tyr	Asn	Asp	Arg	Ser	Val	Leu
		275					280					285			
Glu	Asn	His	His	Val	Ser	Ala	Ala	Tyr	Arg	Leu	Met	Gln	Glu	Glu	Glu
	290					295					300				
Met	Asn	Val	Leu	Ile	Asn	Leu	Ser	Lys	Asp	Asp	Trp	Arg	Asp	Leu	Arg
305					310					315					320
Asn	Leu	Val	Ile	Glu	Met	Val	Leu	Ser	Thr	Asp	Met	Ser	Gly	His	Phe
			325						330					335	
Gln	Gln	Ile	Lys	Asn	Ile	Arg	Asn	Ser	Leu	Gln	Gln	Pro	Glu	Gly	Leu
			340					345					350		
Asp	Lys	Ala	Lys	Thr	Met	Ser	Leu	Ile	Leu	His	Ala	Ala	Asp	Ile	Ser
		355					360					365			
His	Pro	Ala	Lys	Ser	Trp	Lys	Leu	His	His	Arg	Trp	Thr	Met	Ala	Leu
	370					375					380				
Met	Glu	Glu	Phe	Phe	Leu	Gln	Gly	Asp	Lys	Glu	Ala	Glu	Leu	Gly	Leu
385					390					395					400
Pro	Phe	Ser	Pro	Leu	Cys	Asp	Arg	Lys	Ser	Thr	Met	Val	Ala	Gln	Ser
			405						410					415	
Gln	Ile	Gly	Phe	Ile	Asp	Phe	Ile	Val	Glu	Pro	Thr	Phe	Ser	Leu	Leu
			420					425					430		
Thr	Asp	Ser	Thr	Glu	Lys	Ile	Ile	Ile	Pro	Leu	Ile	Glu	Glu	Asp	Ser
		435					440					445			
Lys	Thr	Lys	Thr	Pro	Ser	Tyr	Gly	Ala	Ser	Arg	Arg	Ser	Asn	Met	Lys
	450					455					460				
Gly	Thr	Thr	Asn	Asp	Gly	Thr	Tyr	Ser	Pro	Asp	Tyr	Ser	Leu	Ala	Ser
465					470					475					480
Val	Asp	Leu	Lys	Ser	Phe	Lys	Asn	Ser	Leu	Val	Asp	Ile	Ile	Gln	Gln
			485						490					495	
Asn	Lys	Glu	Arg	Trp	Lys	Glu	Leu	Ala	Ala	Gln	Gly	Glu	Pro	Asp	Pro
			500					505					510		

His Lys Asn Ser Asp Leu Val Asn Ala Glu Glu Lys His Ala Glu Thr
515 520 525

His Ser
530

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Asp Asp His Val Thr Ile
1 5

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATGAGRAGRC AYGTHACNAT

20

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Leu Arg Cys Leu Val Lys Gln
1 5

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CTGCTTCACT AAGCATCTTA G

21

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 75 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATGAGAAGGC ACGTAACGAT CAGGAGGAAA CATCTCCAAA GACCCATCTT TAGACTAAGA
TGCTTAGTGA AGCAG

60

75

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATGGAYGAYC ACGTAACGAT C

21

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AAGTATCTCA TTGGAGAACA G

21

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 54 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ATGGATGATC ACGTAACGAT CAGGAGGAAA CATCTCCAAA GACCCATCTT TAGA

54

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met Asp Asp His Val Thr Ile Arg Arg Lys His Leu Gln Arg Pro Ile
 1 5 10 15

Phe Arg

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2656 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 136..1677

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TTGCTGTCGA GAGAAAGAGG AAACACTTTT TGCCTTCTGG GTCCTTGCA GGACAATAGA	60
TCAGGATAAG CTTCCACATT CTCTCCCTGG ATTTCTGGAG TGGTTTCCAG GAACAAGCTA	120
AACTTTCACC TTAA ATG GAT GAC CAT GTC ACA ATC AGG AGG AAA CAT CTC	171
Met Asp Asp His Val Thr Ile Arg Arg Lys His Leu	
1 5 10	
CAA AGA CCC ATC TTT AGA CTA AGA TGC TTA GTG AAG CAG CTG GAA AAA	219
Gln Arg Pro Ile Phe Arg Leu Arg Cys Leu Val Lys Gln Leu Glu Lys	
15 20 25	
GGT GAT GTT AAC GTC ATC GAC TTA AAG AAG AAT ATT GAA TAT GCA GCA	267
Gly Asp Val Asn Val Ile Asp Leu Lys Lys Asn Ile Glu Tyr Ala Ala	
30 35 40	
TCT GTG TTG GAA GCA GTT TAT ATT GAT GAA ACA AGG AGA CTG CTG GAC	315
Ser Val Leu Glu Ala Val Tyr Ile Asp Glu Thr Arg Arg Leu Leu Asp	
45 50 55 60	
ACC GAT GAT GAG CTC AGT GAC ATT CAG TCG GAT TCC GTC CCA TCA GAA	363
Thr Asp Asp Glu Leu Ser Asp Ile Gln Ser Asp Ser Val Pro Ser Glu	
65 70 75	

GTC Val	CGG Arg	GAC Asp	TGG Trp	TTG Leu	GCT Ala	TCT Ser	ACC Thr	TTT Phe	ACA Thr	CGG Arg	AAA Lys	ATG Met	GGG Gly	ATG Met	ATG Met	411
			80					85					90			
AAA Lys	AAG Lys	AAA Lys	TCT Ser	GAG Glu	GAA Glu	AAA Lys	CCA Pro	AGA Arg	TTT Phe	CGG Arg	AGC Ser	ATT Ile	GTG Val	CAT His	GTT Val	459
		95					100					105				
GTT Val	CAA Gln	GCT Ala	GGA Gly	ATT Ile	TTT Phe	GTG Val	GAA Glu	AGA Arg	ATG Met	TAC Tyr	AGA Arg	AAG Lys	TCC Ser	TAT Tyr	CAC His	507
	110					115				120						
ATG Met	GTT Val	GGC Gly	TTG Leu	GCA Ala	TAT Tyr	CCA Pro	GAG Glu	GCT Ala	GTC Val	ATA Ile	GTA Val	ACA Thr	TTA Leu	AAG Lys	GAT Asp	555
125					130				135						140	
GTT Val	GAT Asp	AAA Lys	TGG Trp	TCT Ser	TTT Phe	GAT Asp	GTA Val	TTT Phe	GCC Ala	TTG Leu	AAT Asn	GAA Glu	GCA Ala	AGT Ser	GGA Gly	603
				145					150					155		
GAA Glu	CAC His	AGT Ser	CTG Leu	AAG Lys	TTT Phe	ATG Met	ATT Ile	TAT Tyr	GAA Glu	CTA Leu	TTC Phe	ACC Thr	AGA Arg	TAT Tyr	GAT Asp	651
			160					165					170			
CTT Leu	ATC Ile	AAC Asn	CGT Arg	TTC Phe	AAG Lys	ATT Ile	CCT Pro	GTT Val	TCT Ser	TGC Cys	CTA Leu	ATT Ile	GCC Ala	TTT Phe	GCA Ala	699
		175					180					185				
GAA Glu	GCT Ala	CTA Leu	GAA Glu	GTT Val	GGT Gly	TAC Tyr	AGC Ser	AAG Lys	TAC Tyr	AAA Lys	AAT Asn	CCA Pro	TAC Tyr	CAC His	AAT Asn	747
	190					195					200					
TTG Leu	ATT Ile	CAT His	GCA Ala	GCT Ala	GAT Asp	GTC Val	ACT Thr	CAA Gln	ACT Thr	GTG Val	CAT His	TAC Tyr	ATA Ile	ATG Met	CTT Leu	795
205					210					215					220	
CAT His	ACA Thr	GGT Gly	ATC Ile	ATG Met	CAC His	TGG Trp	CTC Leu	ACT Thr	GAA Glu	CTG Leu	GAA Glu	ATT Ile	TTA Leu	GCA Ala	ATG Met	843
				225					230					235		
GTC Val	TTT Phe	GCC Ala	GCT Ala	GCC Ala	ATT Ile	CAT His	GAC Asp	TAT Tyr	GAG Glu	CAT His	ACA Thr	GGG Gly	ACT Thr	ACA Thr	AAC Asn	891
		240					245					250				
AAT Asn	TTT Phe	CAC His	ATT Ile	CAG Gln	ACA Thr	AGG Arg	TCA Ser	GAT Asp	GTT Val	GCC Ala	ATT Ile	TTG Leu	TAT Tyr	AAT Asn	GAT Asp	939
		255					260					265				
CGC Arg	TCT Ser	GTC Val	CTT Leu	GAA Glu	AAT Asn	CAT His	CAT His	GTG Val	AGT Ser	GCA Ala	GCT Ala	TAT Tyr	CGC Arg	CTT Leu	ATG Met	987
	270					275				280						
CAA Gln	GAA Glu	GAA Glu	GAA Glu	ATG Met	AAT Asn	GTC Val	CTG Leu	ATA Ile	AAT Asn	TTA Leu	TCC Ser	AAA Lys	GAT Asp	GAC Asp	TGG Trp	1035
285					290					295					300	
AGG Arg	GAT Asp	CTT Leu	CGG Arg	AAC Asn	CTA Leu	GTG Val	ATT Ile	GAA Glu	ATG Met	GTG Val	TTG Leu	TCT Ser	ACA Thr	GAC Asp	ATG Met	1083
				305					310					315		
TCG Ser	GGT Gly	CAC His	TTC Phe	CAG Gln	CAA Gln	ATT Ile	AAA Lys	AAT Asn	ATA Ile	AGA Arg	AAT Asn	AGT Ser	TTG Leu	CAG Gln	CAA Gln	1131
			320				325						330			
CCT Pro	GAA Glu	GGG Gly	CTT Leu	GAC Asp	AAA Lys	GCC Ala	AAA Lys	ACC Thr	ATG Met	TCC Ser	CTG Leu	ATT Ile	CTC Leu	CAT His	GCA Ala	1179
		335					340					345				

GCA GAC ATC AGT CAC CCA GCC AAA TCC TGG AAG CTG CAC CAC CGA TGG Ala Asp Ile Ser His Pro Ala Lys Ser Trp Lys Leu His His Arg Trp 350 355 360	1227
ACC ATG GCC CTA ATG GAG GAG TTT TTC CTA CAG GGA GAT AAA GAA GCT Thr Met Ala Leu Met Glu Glu Phe Phe Leu Gln Gly Asp Lys Glu Ala 365 370 375 380	1275
GAA TTA GGG CTT CCA TTT TCC CCG CTT TGC GAT CGG AAG TCA ACG ATG Glu Leu Gly Leu Pro Phe Ser Pro Leu Cys Asp Arg Lys Ser Thr Met 385 390 395	1323
GTG GCC CAG TCC CAA ATA GGT TTC ATT GAT TTC ATA GTA GAA CCA ACA Val Ala Gln Ser Gln Ile Gly Phe Ile Asp Phe Ile Val Glu Pro Thr 400 405 410	1371
TTT TCT CTT CTG ACA GAC TCA ACA GAG AAA ATT ATT ATT CCT CTT ATA Phe Ser Leu Leu Thr Asp Ser Thr Glu Lys Ile Ile Ile Pro Leu Ile 415 420 425	1419
GAG GAA GAC TCG AAA ACC AAA ACT CCT TCC TAT GGA GCA AGC AGA CGA Glu Glu Asp Ser Lys Thr Lys Thr Pro Ser Tyr Gly Ala Ser Arg Arg 430 435 440	1467
TCA AAT ATG AAA GGC ACC ACC AAT GAT GGA ACC TAC TCC CCC GAC TAC Ser Asn Met Lys Gly Thr Thr Asn Asp Gly Thr Tyr Ser Pro Asp Tyr 445 450 455 460	1515
TCC CTT GCC AGC GTG GAC CTG AAG AGC TTC AAA AAC AGC CTG GTG GAC Ser Leu Ala Ser Val Asp Leu Lys Ser Phe Lys Asn Ser Leu Val Asp 465 470 475	1563
ATC ATC CAG CAG AAC AAA GAG AGG TGG AAA GAG TTA GCT GCT CAA GGT Ile Ile Gln Gln Asn Lys Glu Arg Trp Lys Glu Leu Ala Ala Gln Gly 480 485 490	1611
GAA CCT GAT CCC CAT AAG AAC TCA GAT CTA GTA AAT GCT GAA GAA AAA Glu Pro Asp Pro His Lys Asn Ser Asp Leu Val Asn Ala Glu Glu Lys 495 500 505	1659
CAT GCT GAA ACA CAT TCA TAGGTCTGAA ACACCTGAAA GACGTCTTTC His Ala Glu Thr His Ser 510	1707
ATTCTAAGGA TGGGAGAGTG CTGTA ACTAC AAAACTTTCA AGCTTCTAAG TAAAAGGAAA	1767
GCAAAAACAA AATTACAGAA AAATATTTTT GCAGCTCTGA GGCTATTTAG ATTGTCCTTG	1827
TTGTTTTTAAA TACATGGGAA CCAAGTGAGA AGAGGGGCTG CTCAGAAGTT GTAGTCGAAG	1887
TCCTAAGACA ACAATGAAGC ATCAGAGCCC TGACTCTGTG ACCTGATGAA CTCTTCGTTG	1947
TAACTCTCAA GCTGGGAAAC CACAGCGAAT CCTGTTCTCTG AAAGCAGTGA ACCAGCCTGC	2007
ATCCACCACT GTTATTGCAA AGCAGCAAAG CATCACCCAC GTGGGGGTCA TCACAATGCA	2067
AGTCACGCAA GACCTATGAC CAAGATGACA AGAACCTCCA GCCCTTGTTG GAGACAGACA	2127
CTAGA ACTGA GAGTGGGATT TGCCTTCTGG GGTGTTAATC CCATCAGGAT GTAACAAAAT	2187
ATATTACAGG TCAAGGGATA AGGGACAAGA AGTGTGTGTC TGTGTGTGTG TGTGTGTATG	2247
TGCGCGCACT CAAAATGTC TGTGAAAATG GAAGCCCAACA CTCTTCTGCA CAGAGAGCAT	2307
TATTTGATGT GATTTATAAT TTTACTACAA ACAAACGAAC TGCAGCCATT GGAGACTGCT	2367
TCCTTGTCAT GTTTTGCTG AGCATGTGCA GAGCCTTGCC TTTGTTCCAA ATTGAAGAAC	2427

TACCTTTATT TGTTATTAGC TGCCAAGAAA GGTCAAGCCC AAGTAGGTGT TGTCATTTTC	2487
ACCGTACAAA CTCTTCAATG ATTGTTAGAC TAAAGGAATT TGTTTTTG TG AAAGGTAGAA	2547
ATTAGATGGA AAAGATCAAG AGTAGTCATC AATTAAAGAA GAAAGTGAAG GTGGATATGT	2607
CCATCCTAAT GAGTTTTCTG TTGCACCTGC TTCTTCCCTG CGACAGCAA	2656

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 514 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met	Asp	Asp	His	Val	Thr	Ile	Arg	Arg	Lys	His	Leu	Gln	Arg	Pro	Ile	1	5	10	15
Phe	Arg	Leu	Arg	Cys	Leu	Val	Lys	Gln	Leu	Glu	Lys	Gly	Asp	Val	Asn	20	25	30	
Val	Ile	Asp	Leu	Lys	Lys	Asn	Ile	Glu	Tyr	Ala	Ala	Ser	Val	Leu	Glu	35	40	45	
Ala	Val	Tyr	Ile	Asp	Glu	Thr	Arg	Arg	Leu	Leu	Asp	Thr	Asp	Asp	Glu	50	55	60	
Leu	Ser	Asp	Ile	Gln	Ser	Asp	Ser	Val	Pro	Ser	Glu	Val	Arg	Asp	Trp	65	70	75	80
Leu	Ala	Ser	Thr	Phe	Thr	Arg	Lys	Met	Gly	Met	Met	Lys	Lys	Lys	Ser	85	90	95	
Glu	Glu	Lys	Pro	Arg	Phe	Arg	Ser	Ile	Val	His	Val	Val	Gln	Ala	Gly	100	105	110	
Ile	Phe	Val	Glu	Arg	Met	Tyr	Arg	Lys	Ser	Tyr	His	Met	Val	Gly	Leu	115	120	125	
Ala	Tyr	Pro	Glu	Ala	Val	Ile	Val	Thr	Leu	Lys	Asp	Val	Asp	Lys	Trp	130	135	140	
Ser	Phe	Asp	Val	Phe	Ala	Leu	Asn	Glu	Ala	Ser	Gly	Glu	His	Ser	Leu	145	150	155	160
Lys	Phe	Met	Ile	Tyr	Glu	Leu	Phe	Thr	Arg	Tyr	Asp	Leu	Ile	Asn	Arg	165	170	175	
Phe	Lys	Ile	Pro	Val	Ser	Cys	Leu	Ile	Ala	Phe	Ala	Glu	Ala	Leu	Glu	180	185	190	
Val	Gly	Tyr	Ser	Lys	Tyr	Lys	Asn	Pro	Tyr	His	Asn	Leu	Ile	His	Ala	195	200	205	
Ala	Asp	Val	Thr	Gln	Thr	Val	His	Tyr	Ile	Met	Leu	His	Thr	Gly	Ile	210	215	220	
Met	His	Trp	Leu	Thr	Glu	Leu	Glu	Ile	Leu	Ala	Met	Val	Phe	Ala	Ala	225	230	235	240
Ala	Ile	His	Asp	Tyr	Glu	His	Thr	Gly	Thr	Thr	Asn	Asn	Phe	His	Ile	245	250	255	

Gln Thr Arg Ser Asp Val Ala Ile Leu Tyr Asn Asp Arg Ser Val Leu
260 265 270

Glu Asn His His Val Ser Ala Ala Tyr Arg Leu Met Gln Glu Glu Glu
275 280 285

Met Asn Val Leu Ile Asn Leu Ser Lys Asp Asp Trp Arg Asp Leu Arg
290 295 300

Asn Leu Val Ile Glu Met Val Leu Ser Thr Asp Met Ser Gly His Phe
305 310 315 320

Gln Gln Ile Lys Asn Ile Arg Asn Ser Leu Gln Gln Pro Glu Gly Leu
325 330 335

Asp Lys Ala Lys Thr Met Ser Leu Ile Leu His Ala Ala Asp Ile Ser
340 345 350

His Pro Ala Lys Ser Trp Lys Leu His His Arg Trp Thr Met Ala Leu
355 360 365

Met Glu Glu Phe Phe Leu Gln Gly Asp Lys Glu Ala Glu Leu Gly Leu
370 375 380

Pro Phe Ser Pro Leu Cys Asp Arg Lys Ser Thr Met Val Ala Gln Ser
385 390 395 400

Gln Ile Gly Phe Ile Asp Phe Ile Val Glu Pro Thr Phe Ser Leu Leu
405 410 415

Thr Asp Ser Thr Glu Lys Ile Ile Ile Pro Leu Ile Glu Glu Asp Ser
420 425 430

Lys Thr Lys Thr Pro Ser Tyr Gly Ala Ser Arg Arg Ser Asn Met Lys
435 440 445

Gly Thr Thr Asn Asp Gly Thr Tyr Ser Pro Asp Tyr Ser Leu Ala Ser
450 455 460

Val Asp Leu Lys Ser Phe Lys Asn Ser Leu Val Asp Ile Ile Gln Gln
465 470 475 480

Asn Lys Glu Arg Trp Lys Glu Leu Ala Ala Gln Gly Glu Pro Asp Pro
485 490 495

His Lys Asn Ser Asp Leu Val Asn Ala Glu Glu Lys His Ala Glu Thr
500 505 510

His Ser

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ATHCAYGAYT AYGARCAYAC NGG

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Ile His Asp Tyr Glu His Thr Gly
1 5

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TCYTTTRTCNC CYTGNCGRAA RAAATCYTCC AT

32

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met Glu Glu Phe Phe Arg Gln Gly Asp Lys Glu
1 5 10

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 412 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..412

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ATT CAT GAT TAT AAC ACA CGG GGC ACT ACC AAC AGC TTC CAC ATC CAG Ile His Asp Tyr Asn Thr Arg Gly Thr Thr Asn Ser Phe His Ile Gln 1 5 10 15	48
ACC AAA TCG GAA TGC GCC ATC CTG TAC AAC GAC CGC TCA GTG CTG GAG Thr Lys Ser Glu Cys Ala Ile Leu Tyr Asn Asp Arg Ser Val Leu Glu 20 25 30	96
AAT CAC CAC ATC AGC TCG GTT TTC CGA ATG ATG CAG GAC GAC GAC ATG Asn His His Ile Ser Ser Val Phe Arg Met Met Gln Asp Asp Asp Met 35 40 45	144
AAC ATC TTC ATC AAC CTC ACC AAG GAT GAG TTT GTA GAG CTG CGG GCT Asn Ile Phe Ile Asn Leu Thr Lys Asp Glu Phe Val Glu Leu Arg Ala 50 55 60	192
CTG GTC ATT GAG ATG GTG TTG GCC ACA GAC ATG TCC TGC CAT TTC CAG Leu Val Ile Glu Met Val Leu Ala Thr Asp Met Ser Cys His Phe Gln 65 70 75 80	240
CAA GTG AAG TCC ATG AAG ACA GCC TTG CAG CAG CTG GAG AGG ATT GAC Gln Val Lys Ser Met Lys Thr Ala Leu Gln Gln Leu Glu Arg Ile Asp 85 90 95	288
AAG TCC AAG GCC CTC TCT CTG CTG CTT CAT GCT GCT GAC ATC AGC CAC Lys Ser Lys Ala Leu Ser Leu Leu Leu His Ala Ala Asp Ile Ser His 100 105 110	336
CCC ACC AAG CAG TGG TCG GTT CAC AGC CGC TGG ACC AAG GCC CTC ATG Pro Thr Lys Gln Trp Ser Val His Ser Arg Trp Thr Lys Ala Leu Met 115 120 125	384
GAG GAG TTC TTC CGA CAA GGG GAC AAA G Glu Glu Phe Phe Arg Gln Gly Asp Lys 130 135	412

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 137 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Ile His Asp Tyr Asn Thr Arg Gly Thr Thr Asn Ser Phe His Ile Gln 1 5 10 15
Thr Lys Ser Glu Cys Ala Ile Leu Tyr Asn Asp Arg Ser Val Leu Glu 20 25 30
Asn His His Ile Ser Ser Val Phe Arg Met Met Gln Asp Asp Asp Met 35 40 45
Asn Ile Phe Ile Asn Leu Thr Lys Asp Glu Phe Val Glu Leu Arg Ala 50 55 60
Leu Val Ile Glu Met Val Leu Ala Thr Asp Met Ser Cys His Phe Gln 65 70 75 80
Gln Val Lys Ser Met Lys Thr Ala Leu Gln Gln Leu Glu Arg Ile Asp 85 90 95

Lys Ser Lys Ala Leu Ser Leu Leu Leu His Ala Ala Asp Ile Ser His
 100 105 110
 Pro Thr Lys Gln Trp Ser Val His Ser Arg Trp Thr Lys Ala Leu Met
 115 120 125
 Glu Glu Phe Phe Arg Gln Gly Asp Lys
 130 135

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

AARAARAAYY TNGARTAYAC NGC

23

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Lys Lys Asn Leu Glu Tyr Thr Ala
 1 5

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1844 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 114..1715

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GGCTGGGCAG CGGGAAGGA GGAGCCGCAG GAACTGCAGC TCTGCCAGCT TGGGCCGAGC
 TTTAGAGACC CCCGGCCTGG CTGGTCCCTG CCAGCCGCAG ACGGAGGCTG AGC ATG
 Met
 1

60

116

GAG CTG TCC CCC CGC AGC CCT CCC GAG ATG CTA GAG TCG GAC TGC CCT Glu Leu Ser Pro Arg Ser Pro Pro Glu Met Leu Glu Ser Asp Cys Pro	164
5 10 15	
TCA CCC CTG GAG CTG AAG TCA GCC CCC AGC AAG AAG ATG TGG ATT AAG Ser Pro Leu Glu Leu Lys Ser Ala Pro Ser Lys Lys Met Trp Ile Lys	212
20 25 30	
CTC CGG TCT CTG CTG CGC TAC ATG GTG AAG CAG TTG GAG AAC GGG GAG Leu Arg Ser Leu Leu Arg Tyr Met Val Lys Gln Leu Glu Asn Gly Glu	260
35 40 45	
GTA AAC ATT GAG GAG CTG AAG AAA AAC CTG GAG TAC ACA GCT TCT CTG Val Asn Ile Glu Glu Tyr Lys Lys Asn Leu Glu Tyr Thr Ala Ser Leu	308
50 55 60 65	
CTG GAG GCC GTC TAT ATA GAT GAG ACT CGG CAA ATC CTG GAC ACG GAG Leu Glu Ala Val Tyr Ile Asp Glu Thr Arg Gln Ile Leu Asp Thr Glu	356
70 75 80	
GAT GAG CTG CAG GAG CTG CGG TCT GAT GCG GTG CCT TCA GAG GTG CGG Asp Glu Leu Gln Glu Leu Arg Ser Asp Ala Val Pro Ser Glu Val Arg	404
85 90 95	
GAC TGG CTG GCC TCC ACC TTC ACC CAG CAG ACC CGG GCC AAA GGC CCG Asp Trp Leu Ala Ser Thr Phe Thr Gln Gln Thr Arg Ala Lys Gly Pro	452
100 105 110	
AGC GAA GAG AAG CCC AAG TTC CGG AGC ATC GTG CAC GCG GTG CAG GCT Ser Glu Glu Lys Pro Lys Phe Arg Ser Ile Val His Ala Val Gln Ala	500
115 120 125	
GGC ATC TTT GTG GAG CGG ATG TTC CGG AGA ACG TAC ACC TCT GTG GGC Gly Ile Phe Val Glu Arg Met Phe Arg Arg Thr Tyr Thr Ser Val Gly	548
130 135 140 145	
CCC ACC TAC TCC ACT GCC GTC CTC AAC TGT CTC AAG AAC GTG GAC CTT Pro Thr Tyr Ser Thr Ala Val Leu Asn Cys Leu Lys Asn Val Asp Leu	596
150 155 160	
TGG TGC TTT GAT GTC TTT TCC TTG AAC CGG GCA GCA GAT GAC CAC GCC Trp Cys Phe Asp Val Phe Ser Leu Asn Arg Ala Ala Asp Asp His Ala	644
165 170 175	
CTG AGG ACC ATC GTT TTT GAG CTG CTG ACT CGG CAC AAC CTC ATC AGC Leu Arg Thr Ile Val Phe Glu Leu Leu Thr Arg His Asn Leu Ile Ser	692
180 185 190	
CGC TTT AAG ATT CCC ACT GTG TTT TTG ATG ACT TTC CTG GAT GCC TTG Arg Phe Lys Ile Pro Thr Val Phe Leu Met Thr Phe Leu Asp Ala Leu	740
195 200 205	
GAG ACA GGC TAC GGA AAG TAC AAG AAC CCT TAC CAC AAC CAG ATC CAC Glu Thr Gly Tyr Gly Lys Tyr Lys Asn Pro Tyr His Asn Gln Ile His	788
210 215 220 225	
GCA GCT GAC GTC ACC CAG ACG GTC CAC TGC TTC TTG CTC CGC ACA GGG Ala Ala Asp Val Thr Gln Thr Val His Cys Phe Leu Leu Arg Thr Gly	836
230 235 240	
ATG GTG CAC TGC CTG TCG GAG ATT GAG GTC CTG GCC ATC ATC TTT GCT Met Val His Cys Leu Ser Glu Ile Glu Val Leu Ala Ile Ile Phe Ala	884
245 250 255	
GCA GCG ATC CAC GAC TAT GAG CAC ACT GGC ACT ACC AAC AGC TTC CAC Ala Ala Ile His Asp Tyr Glu His Thr Gly Thr Thr Asn Ser Phe His	932
260 265 270	

ATC Ile	CAG Gln	ACC Thr	AAA Lys	TCG Ser	GAA Glu	TGC Cys	GCC Ala	ATC Ile	CTG Leu	TAC Tyr	AAC Asn	GAC Asp	CGC Arg	TCA Ser	GTG Val	980
275						280					285					
CTG Leu	GAG Glu	AAT Asn	CAC His	CAC His	ATC Ile	AGC Ser	TCG Ser	GTT Val	TTC Phe	CGA Arg	ATG Met	ATG Met	CAG Gln	GAC Asp	GAC Asp	1028
290					295				300						305	
GAG Glu	ATG Met	AAC Asn	ATC Ile	TTC Phe	ATC Ile	AAC Asn	CTC Leu	ACC Thr	AAG Lys	GAT Asp	GAG Glu	TTT Phe	GTA Val	GAG Glu	CTG Leu	1076
			310						315					320		
CGG Arg	GCT Ala	CTG Leu	GTC Val	ATT Ile	GAG Glu	ATG Met	GTG Val	TTG Leu	GCC Ala	ACA Thr	GAC Asp	ATG Met	TCC Ser	TGC Cys	CAT His	1124
			325					330					335			
TTC Phe	CAG Gln	CAA Gln	GTG Val	AAG Lys	TCC Ser	ATG Met	AAG Lys	ACA Thr	GCC Ala	TTG Leu	CAG Gln	CAG Gln	CTG Leu	GAG Glu	AGG Arg	1172
		340					345					350				
ATT Ile	GAC Asp	AAG Lys	TCC Ser	AAG Lys	GCC Ala	CTC Leu	TCT Ser	CTG Leu	CTG Leu	CTT Leu	CAT His	GCT Ala	GCT Ala	GAC Asp	ATC Ile	1220
	355					360					365					
AGC Ser	CAC His	CCC Pro	ACC Thr	AAG Lys	CAG Gln	TGG Trp	TCG Ser	GTT Val	CAC His	AGC Ser	CGC Arg	TGG Trp	ACC Thr	AAG Lys	GCC Ala	1268
370					375					380					385	
CTC Leu	ATG Met	GAG Glu	GAA Glu	TTC Phe	TTC Phe	CGC Arg	CAG Gln	GGT Gly	GAC Asp	AAG Lys	GAG Glu	GCT Ala	GAG Glu	CTG Leu	GGC Gly	1316
			390						395					400		
CTG Leu	CCC Pro	TTT Phe	TCT Ser	CCG Pro	CTC Leu	TGT Cys	GAC Asp	CGC Arg	ACT Thr	TCC Ser	ACC Thr	CTC Leu	GTG Val	GCG Ala	CAG Gln	1364
			405					410					415			
TCC Ser	CAG Gln	ATT Ile	GGT Gly	TTC Phe	ATC Ile	GAC Asp	TTC Phe	ATT Ile	GTG Val	GAG Glu	CCC Pro	ACG Thr	TTC Phe	TCT Ser	GTG Val	1412
		420					425					430				
CTC Leu	ACC Thr	GAT Asp	GTG Val	GCT Ala	GAG Glu	AAG Lys	AGT Ser	GTC Val	CAG Gln	CCC Pro	ACC Thr	GGG Gly	GAC Asp	GAC Asp	GAC Asp	1460
		435				440					445					
TCG Ser	AAG Lys	TCT Ser	AAA Lys	AAC Asn	CAG Gln	CCC Pro	AGC Ser	TTC Phe	CAG Gln	TGG Trp	CGC Arg	CAG Gln	CCT Pro	TCT Ser	CTG Leu	1508
450					455					460					465	
GAT Asp	GTA Val	GAA Glu	GTG Val	GGA Gly	GAC Asp	CCC Pro	AAC Asn	CCT Pro	GAC Asp	GTG Val	GTC Val	AGC Ser	TTC Phe	CGC Arg	TCC Ser	1556
			470					475						480		
ACC Thr	TGG Trp	ACC Thr	AAA Lys	TAC Tyr	ATT Ile	CAG Gln	GAG Glu	AAC Asn	AAG Lys	CAG Gln	AAA Lys	TGG Trp	AAG Lys	GAA Glu	CGG Arg	1604
			485					490					495			
GCG Ala	GCG Ala	AGC Ser	GGC Gly	ATC Ile	ACC Thr	AAC Asn	CAG Gln	ATG Met	TCC Ser	ATT Ile	GAC Asp	GAA Glu	CTG Leu	TCC Ser	CCT Pro	1652
		500					505					510				
TGT Cys	GAG Glu	GAA Glu	GAG Glu	GCC Ala	CCA Pro	GCC Ala	TCC Ser	CCT Pro	GCC Ala	GAA Glu	GAC Asp	GAG Glu	CAC His	AAC Asn	CAG Gln	1700

CGATGTCATC AGCACCATCC ATCGGGACTG GCTCCCCCAT CTGCTCCGAG GCGGAATGGA 1815
TGTC AAGGAA CAGAAAACCC ACCCGAAGA 1844

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Met	Glu	Leu	Ser	Pro	Arg	Ser	Pro	Pro	Glu	Met	Leu	Glu	Ser	Asp	Cys	1	5	10	15
Pro	Ser	Pro	Leu	Glu	Leu	Lys	Ser	Ala	Pro	Ser	Lys	Lys	Met	Trp	Ile	20	25	30	
Lys	Leu	Arg	Ser	Leu	Leu	Arg	Tyr	Met	Val	Lys	Gln	Leu	Glu	Asn	Gly	35	40	45	
Glu	Val	Asn	Ile	Glu	Glu	Leu	Lys	Lys	Asn	Leu	Glu	Tyr	Thr	Ala	Ser	50	55	60	
Leu	Leu	Glu	Ala	Val	Tyr	Ile	Asp	Glu	Thr	Arg	Gln	Ile	Leu	Asp	Thr	65	70	75	80
Glu	Asp	Glu	Leu	Gln	Glu	Leu	Arg	Ser	Asp	Ala	Val	Pro	Ser	Glu	Val	85	90	95	
Arg	Asp	Trp	Leu	Ala	Ser	Thr	Phe	Thr	Gln	Gln	Thr	Arg	Ala	Lys	Gly	100	105	110	
Pro	Ser	Glu	Lys	Pro	Lys	Phe	Arg	Ser	Ile	Val	His	Ala	Val	Gln		115	120	125	
Ala	Gly	Ile	Phe	Val	Glu	Arg	Met	Phe	Arg	Arg	Thr	Tyr	Thr	Ser	Val	130	135	140	
Gly	Pro	Thr	Tyr	Ser	Thr	Ala	Val	Leu	Asn	Cys	Leu	Lys	Asn	Val	Asp	145	150	155	160
Leu	Trp	Cys	Phe	Asp	Val	Phe	Ser	Leu	Asn	Arg	Ala	Ala	Asp	Asp	His	165	170	175	
Ala	Leu	Arg	Thr	Ile	Val	Phe	Glu	Leu	Leu	Thr	Arg	His	Asn	Leu	Ile	180	185	190	
Ser	Arg	Phe	Lys	Ile	Pro	Thr	Val	Phe	Leu	Met	Thr	Phe	Leu	Asp	Ala	195	200	205	
Leu	Glu	Thr	Gly	Tyr	Gly	Lys	Tyr	Lys	Asn	Pro	Tyr	His	Asn	Gln	Ile	210	215	220	
His	Ala	Ala	Asp	Val	Thr	Gln	Thr	Val	His	Cys	Phe	Leu	Leu	Arg	Thr	225	230	235	240
Gly	Met	Val	His	Cys	Leu	Ser	Glu	Ile	Glu	Val	Leu	Ala	Ile	Ile	Phe	245	250	255	
Ala	Ala	Ala	Ile	His	Asp	Tyr	Glu	His	Thr	Gly	Thr	Thr	Asn	Ser	Phe	260	265	270	

His Il Gln Thr Lys Ser Glu Cys Ala Ile Leu Tyr Asn Asp Arg Ser
 275 280 285
 Val Leu Glu Asn His His Ile Ser Ser Val Phe Arg Met Met Gln Asp
 290 295 300
 Asp Glu Met Asn Ile Phe Ile Asn Leu Thr Lys Asp Glu Phe Val Glu
 305 310 315 320
 Leu Arg Ala Leu Val Ile Glu Met Val Leu Ala Thr Asp Met Ser Cys
 325 330 335
 His Phe Gln Gln Val Lys Ser Met Lys Thr Ala Leu Gln Gln Leu Glu
 340 345 350
 Arg Ile Asp Lys Ser Lys Ala Leu Ser Leu Leu Leu His Ala Ala Asp
 355 360 365
 Ile Ser His Pro Thr Lys Gln Trp Ser Val His Ser Arg Trp Thr Lys
 370 375 380
 Ala Leu Met Glu Glu Phe Phe Arg Gln Gly Asp Lys Glu Ala Glu Leu
 385 390 395 400
 Gly Leu Pro Phe Ser Pro Leu Cys Asp Arg Thr Ser Thr Leu Val Ala
 405 410 415
 Gln Ser Gln Ile Gly Phe Ile Asp Phe Ile Val Glu Pro Thr Phe Ser
 420 425 430
 Val Leu Thr Asp Val Ala Glu Lys Ser Val Gln Pro Thr Gly Asp Asp
 435 440 445
 Asp Ser Lys Ser Lys Asn Gln Pro Ser Phe Gln Trp Arg Gln Pro Ser
 450 455 460
 Leu Asp Val Glu Val Gly Asp Pro Asn Pro Asp Val Val Ser Phe Arg
 465 470 475 480
 Ser Thr Trp Thr Lys Tyr Ile Gln Glu Asn Lys Gln Lys Trp Lys Glu
 485 490 495
 Arg Ala Ala Ser Gly Ile Thr Asn Gln Met Ser Ile Asp Glu Leu Ser
 500 505 510
 Pro Cys Glu Glu Glu Ala Pro Ala Ser Pro Ala Glu Asp Glu His Asn
 515 520 525
 Gln Asn Gly Asn Leu Asp
 530

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Gln Leu Glu Asn Gly Glu Val Asn Ile Glu Glu Leu Lys Lys
 1 5 10

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Gln Leu Ile Pro Gly Arg Val Asn Ile Ile Ser Leu Lys Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Lys Ser Glu Cys Ala Ile Leu Tyr Asn Asp Arg Ser Val Leu Glu Asn
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Lys Asp Glu Thr Ala Ile Leu Tyr Asn Asp Arg Thr Val Leu Glu Asn
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GGATCCGGAT CCCGCAGACG GAGGCTGAGC ATGG

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GGATCCGGAT CCAGGACCTG GCCAGGCCCG GC

32

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Glu Met Met Met Tyr His Met Lys
1 5

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Tyr His Asn Trp Met His Ala Phe
1 5

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

TTCATRTGRT ACATCATCAT YTC

23

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

AANGCRTGCA TCCARTTRTG RTA

23

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4131 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 148..2910

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

AGGCGCAGCG GCCGGGCCCG CGGGCGGGCG GCGGGCTGCG AGCATGGTCC TGGTGCTGCA	60
CCACATCCTC ATCGCTGTTG TCCAATTCTT CAGGCGGGGC CAGCAGGTCT TCCTCAAGCC	120
GGACGAGCCG CCGCCGCCGC CGCAGCC ATG CGC CGA CAG CCT GCA GCC AGC	171
Met Arg Arg Gln Pro Ala Ala Ser	
CGG GAC CTC TTT GCA CAG GAG CCA GTG CCC CCA GGG AGT GGA GAC GGC	219
Arg Asp Leu Phe Ala Gln Glu Pro Val Pro Pro Gly Ser Gly Asp Gly	
GCA TTG CAG GAT GCT TTG CTG AGC CTG GGC TCC GTC ATC GAC GTT GCA	267
Ala Leu Gln Asp Ala Leu Leu Ser Leu Gly Ser Val Ile Asp Val Ala	
GGC TTG CAA CAG GCT GTC AAG GAG GCC CTG TCG GCT GTG CTT CCC AAA	315
Gly Leu Gln Gln Ala Val Lys Glu Ala Leu Ser Ala Val Leu Pro Lys	
GTG GAG ACG GTC TAC ACC TAC CTG CTG GAT GGG GAA TCC CGG CTG GTG	363
Val Glu Thr Val Tyr Thr Tyr Leu Leu Asp Gly Glu Ser Arg Leu Val	
TGT GAG GAG CCC CCC CAC GAG CTG CCC CAG GAG GGG AAA GTG CGA GAG	411
Cys Glu Glu Pro Pro His Glu Leu Pro Gln Glu Gly Lys Val Arg Glu	
GCT GTG ATC TCC CGG AAG CGG CTG GGC TGC AAT GGA CTG GGC CCC TCA	459
Ala Val Ile Ser Arg Lys Arg Leu Gly Cys Asn Gly Leu Gly Pr S r	

GAC CTG CCT GGG AAG CCC TTG GCA AGG CTG GTG GCT CCA CTG GCT CCT Asp Leu Pro Gly Lys Pro Leu Ala Arg Leu Val Ala Pro Leu Ala Pro 105 110 115 120	507
GAC ACC CAA GTG CTG GTC ATA CCG CTG GTG GAC AAG GAG GCC GGG GCT Asp Thr Gln Val Leu Val Ile Pro Leu Val Asp Lys Glu Ala Gly Ala 125 130 135	555
GTG GCA GCT GTC ATC TTG GTG CAC TGT GGT CAG CTG AGT GAC AAT GAG Val Ala Ala Val Ile Leu Val His Cys Gly Gln Leu Ser Asp Asn Glu 140 145 150	603
GAG TGG AGC CTG CAA GCT GTG GAG AAG CAT ACC CTG GTG GCC CTG AAA Glu Trp Ser Leu Gln Ala Val Glu Lys His Thr Leu Val Ala Leu Lys 155 160 165	651
AGG GTG CAG GCC TTG CAG CAG CGC GAG TCC AGC GTG GCC CCG GAA GCG Arg Val Gln Ala Leu Gln Gln Arg Glu Ser Ser Val Ala Pro Glu Ala 170 175 180	699
ACC CAG AAT CCT CCG GAG GAG GCA GCG GGA GAC CAG AAG GGT GGG GTC Thr Gln Asn Pro Pro Glu Glu Ala Ala Gly Asp Gln Lys Gly Gly Val 185 190 200	747
GCA TAC ACA AAC CAA GAC CGA AAG ATC CTG CAG CTT TGC GGG GAG CTC Ala Tyr Thr Asn Gln Asp Arg Lys Ile Leu Gln Leu Cys Gly Glu Leu 205 210 215	795
TAC GAC CTG GAT GCA TCT TCC CTG CAG CTC AAA GTC CTC CAA TAT CTG Tyr Asp Leu Ala Ser Ser Leu Gln Leu Lys Val Leu Gln Tyr Leu 220 225 230	843
CAA CAG GAG ACC CAG GCA TCC CGC TGC TGC CTG CTG CTG GTA TCC GAG Gln Gln Glu Thr Gln Ala Ser Cys Cys Leu Leu Leu Val Ser Glu 235 240 245	891
GAC AAT CTT CAG CTC TCC TGC AAG GTC ATT GGA GAT AAA GTA CTG GAG Asp Asn Leu Gln Leu Ser Cys Lys Val Ile Gly Asp Lys Val Leu Glu 250 255 260	939
GAA GAG ATC AGC TTT CCG TTG ACC ACA GGA CGC CTG GGC CAA GTG GTG Glu Glu Ile Ser Phe Pro Leu Thr Thr Gly Arg Leu Gly Gln Val Val 265 270 275 280	987
GAA GAC AAG AAG TCT ATC CAG CTG AAA GAT CTC ACC TCC GAG GAT ATG Gln Asp Lys Lys Ser Ile Gln Leu Lys Asp Leu Thr Ser Glu Asp Met 285 290 295	1035
CAA CAG CTG CAA AGC ATG TTG GGC TGT GAG GTG CAG GCC ATG CTC TGT Gln Gln Leu Gln Ser Met Leu Gly Cys Glu Val Gln Ala Met Leu Cys 300 305 310	1083
GTC CCT GTC ATC AGC CGG GCC ACT GAC CAG GTC GTG GCC CTG GCC TGT Val Pro Val Ile Ser Arg Ala Thr Asp Gln Val Val Ala Leu Ala Cys 315 320 325	1131
GCC TTC AAC AAG CTC GGA GGA GAC TTG TTC ACA GAC CAG GAC GAG CAC Ala Phe Asn Lys Leu Gly Gly Asp Leu Phe Thr Asp Gln Asp Glu His 330 335 340	1179
GTG ATC CAG CAC TGC TTC CAC TAC ACC AGC ACA GTG CTC ACC AGC ACC Val Ile Gln His Cys Phe His Tyr Thr Ser Thr Val Leu Thr Ser Thr 345 350 355 360	1227
CTG GCC TTC CAG AAG GAG CAG AAG CTC AAG TGT GAG TGC CAG GCT CTT Leu Ala Phe Gln Lys Glu Gln Lys Leu Lys Cys Glu Cys Gln Ala Leu 365 370 375	1275

CTC CAA GTG GCG AAG AAC CTC TTC ACT CAT CTG GAT GAC GTC TCC GTG Leu Gln Val Ala Lys Asn Leu Phe Thr His Leu Asp Asp Val Ser Val 380 385 390	1323
CTG CTC CAG GAG ATC ATC ACA GAG GCC AGG AAC CTC AGC AAT GCT GAG Leu Leu Gln Glu Ile Ile Thr Glu Ala Arg Asn Leu Ser Asn Ala Glu 395 400 405	1371
ATC TGC TCT GTG TTC CTG CTG GAT CAG AAC GAG CTG GTG GCC AAG GTG Ile Cys Ser Val Phe Leu Leu Asp Gln Asn Glu Leu Val Ala Lys Val 410 415 420	1419
TTC GAT GGG GGT GTG GTG GAA GAT GAG AGC TAT GAG ATC CGC ATT CCC Phe Asp Gly Gly Val Val Glu Asp Glu Ser Tyr Glu Ile Arg Ile Pro 425 430 435 440	1467
GCT GAC CAG GGC ATC GCG GGT CAT GTG GCG ACC ACC GGC CAG ATC CTA Ala Asp Gln Gly Ile Ala Gly His Val Ala Thr Thr Gly Gln Ile Leu 445 450 455	1515
AAC ATC CCA GAT GCT TAC GCA CAT CCG CTT TTC TAC CGA GGC GTG GAC Asn Ile Pro Asp Ala Tyr Ala His Pro Leu Phe Tyr Arg Gly Val Asp 460 465 470	1563
GAC AGC ACC GGC TTC CGG ACG CGC AAC ATC CTC TGC TTC CCC ATC AAG Asp Ser Thr Gly Phe Arg Thr Arg Asn Ile Leu Cys Phe Pro Ile Lys 475 480 485	1611
AAC GAG AAC CAG GAG GTC ATC GGT GTG GCC GAG CTG GTG AAC AAG ATC Asn Glu Asn Gln Glu Val Ile Gly Val Ala Glu Leu Val Asn Lys Ile 490 495 500	1659
AAT GGA CCA TGG TTC AGC AAG TTT GAT GAA GAC CTG GCT ACA GCC TTC Asn Gly Pro Trp Phe Ser Lys Phe Asp Glu Asp Leu Ala Thr Ala Phe 505 510 515 520	1707
TCC ATC TAC TGT GGC ATC AGC ATT GCC CAT TCC CTC CTA TAC AAG AAA Ser Ile Tyr Cys Gly Ile Ser Ile Ala His Ser Leu Leu Tyr Lys Lys 525 530 535	1755
GTG AAT GAG GCG CAG TAT CGC AGC CAC CTT GCC AAT GAG ATG ATG ATG Val Asn Glu Ala Gln Tyr Arg Ser His Leu Ala Asn Glu Met Met Met 540 545 550	1803
TAC CAC ATG AAG GTC TCT GAT GAC GAG TAC ACC AAA CTT CTC CAT GAC Tyr His Met Lys Val Ser Asp Asp Glu Tyr Thr Lys Leu Leu His Asp 555 560 565	1851
GGG ATC CAG CCT GTG GCT GCC ATC GAC TCC AAC TTT GCC AGT TTC ACA Gly Ile Gln Pro Val Ala Ala Ile Asp Ser Asn Phe Ala Ser Phe Thr 570 575 580	1899
TAC ACT CCT CGC TCT CTG CCC GAG GAT GAC ACT TCC ATG GCC ATC CTG Tyr Thr Pro Arg Ser Leu Pro Glu Asp Asp Thr Ser Met Ala Ile Leu 585 590 595 600	1947
AGC ATG CTG CAG GAC ATG AAT TTC ATC AAT AAC TAC AAA ATT GAC TGC Ser Met Leu Gln Asp Met Asn Phe Ile Asn Asn Tyr Lys Ile Asp Cys 605 610 615	1995
CCG ACA CTG GCC CGG TTC TGT TTG ATG GTG AAG AAG GGC TAC CGG GAT Pro Thr Leu Ala Arg Phe Cys Leu Met Val Lys Lys Gly Tyr Arg Asp 620 625 630	2043
CCC CCC TAC CAC AAC TGG ATG CAC GCC TTT TCT GTC TCC CAC TTC TGC Pro Pro Tyr His Asn Trp Met His Ala Phe Ser Val Ser His Phe Cys 635 640 645	2091

TAC Tyr 650	CTG Leu	CTC Leu	TAC Tyr	AAG Lys	AAC Asn	CTG Leu 655	GAG Glu	CTC Leu	ACC Thr	AAC Asn	TAC Tyr 660	CTC Leu	GAG Glu	GAC Asp	ATG Met	2139
GAG Glu 665	ATC Ile	TTT Phe	GCC Ala	TTG Leu	TTT Phe 670	ATT Ile	TCC Ser	TGC Cys	ATG Met	TGT Cys 675	CAC His	GAC Asp	CTG Leu	GAC Asp	CAC His 680	2187
AGA Arg	GGC Gly	ACA Thr	AAC Asn	AAC Asn 685	TCC Ser	TTC Phe	CAG Gln	GTG Val	GCC Ala 690	TCG Ser	AAA Lys	TCT Ser	GTG Val	CTG Leu 695	GCC Ala	2235
GCG Ala	CTC Leu	TAC Tyr	AGC Ser 700	TCG Ser	GAA Glu	GGC Gly	TCT Ser	GTC Val 705	ATG Met	GAG Glu	AGG Arg	CAC His 710	CAC His 710	TTC Phe	GCT Ala	2283
CAG Gln	GCC Ala	ATT Ile 715	GCC Ala	ATC Ile	CTC Leu	AAC Asn	ACC Thr 720	CAC His	GGC Gly	TGC Cys	AAC Asn 725	ATC Ile	TTT Phe	GAC Asp	CAC His	2331
TTC Phe 730	TCC Ser	CGG Arg	AAG Lys	GAT Asp	TAT Tyr	CAG Gln 735	CGC Arg	ATG Met	TTG Leu	GAC Asp 740	CTG Leu	ATG Met	CGG Arg	GAC Asp	ATC Ile	2379
ATC Ile 745	TTG Leu	GCC Ala	ACA Thr	GAT Asp 750	CTG Leu	GCC Ala	CAC His	CAC His	CTC Leu	CGC Arg 755	ATC Ile	TTC Phe	AAG Lys	GAC Asp	CTC Leu 760	2427
CAA Gln	AAG Lys	ATG Met	GCC Ala	GAA Glu 765	GTG Val	GGC Gly	TAT Tyr	GAT Asp 770	CGA Arg	ACC Thr	AAC Asn	AAG Lys	CAG Gln	CAC His 775	CAC His	2475
AGC Ser	CTC Leu	CTT Leu 780	CTC Cys	TGC Leu	CTC Leu	CTT Leu	ATG Met	ACC Thr 785	TCC Ser	TGT Cys	GAC Asp	CTC Leu	TCT Ser 790	GAC Asp	CAG Gln	2523
ACC Thr	AAG Lys 795	GGC Gly	TGG Trp	AAG Lys	ACC Thr	ACG Thr	AGG Arg 800	AAG Lys	ATC Ile	GCG Ala	GAG Glu	CTG Leu 805	ATC Ile	TAC Tyr	AAA Lys	2571
GAG Glu 810	TTC Phe	TTC Ser	TCC Gln	CAG Gly	GGA Glu 815	GAC Asp	TTG Leu	GAG Glu	AAG Lys	GCC Ala	ATG Met 820	GGC Gly	AAC Asn	AGG Arg	CCG Pro	2619
ATG Met 825	GAG Glu	ATG Met	ATG Met	GAC Asp 830	CGT Arg	GAG Glu	AAG Lys	GCC Ala	TAC Tyr	ATC Ile 835	CCC Pro	GAG Glu	CTG Leu	CAG Gln	ATC Ile 840	2667
AGC Ser	TTC Phe	ATG Met	GAG Glu 845	CAC His	ATC Ile	GCA Ala	ATG Met	CCC Pro	ATC Ile 850	TAC Tyr	AAG Lys	CTG Leu	CTG Leu	CAA Gln 855	GAC Asp	2715
CTG Leu	TTC Phe	CCC Pro	AAG Lys 860	GCG Ala	GCC Ala	GAG Glu	TTG Leu	TAC Tyr 865	GAA Glu	CGC Arg	GTG Val	GCC Ala	TCT Ser 870	AAT Asn	CGT Arg	2763
GAG Glu	CAC His 875	TGG Thr	ACC Lys	AAG Val	GTG Ser	TCA Ser	CAC His 880	AAG Lys	TTC Phe	ACC Thr	ATC Ile	CGA Arg 885	GGC Gly	CTC Leu	CCG Pro	2811
AGC Ser	AAC Asn 890	AAC Ser	TCG Leu	TTG Asp	GAC Phe 895	TTC Leu	CTG Asp	GAG Glu	GAG Glu	TAT Tyr 900	GAG Glu	GTG Val	CCT Pro	GAC Asp		2859
CTG Leu 905	GAT Asp	GGC Gly	GCT Ala	AGG Arg	GCT Ala 910	CCC Pro	ATC Ile	AAT Asn	GGC Gly	TGT Cys 915	TGC Cys	AGC Ser	CTT Leu	GAT Asp	GCT Ala 920	2907

GAG TGAGTCCCTC CTGGGACCCC TCCCTGTCCA GGCCTCCTCC CACAAGCCTC Glu	2960
CACGGGCCTG GCCGCACGCC CTGGGACCAG AGCCAAGGGT CCTGGATTCT AGGCCAGGAC	3020
TTCCCATGTG ACCCGGGCGA GGTCTGACCT TCCCGGGCCT CAGCTTTCTT GTCTGTATAA	3080
TGGAAGACTT CAGCCTCACT GAGACTTTGT CACTTGTCTT CTGAGAGCAC AGGGGTAACC	3140
AATGAGCAGT GGACCCTGCT CTGCACCTCT GACCGCATCT TGGCAAGTCC CCACCCTCCA	3200
GGCCACTCCT TCTCTGAGGC AGCCGGATGG TTTCTTCTGG GCCCCATTCC TGCCCTACCA	3260
GACCTGTGCC CTTTCCTGTG GGGGCACCTT CACTGGCTCC CAGGATCCTC AGGCAAGAAC	3320
ATGAGACATC TGAGTGGGCA AAGGGTGGGT CTTAGAGACA GTTATCAGCC TGGCTGGAGG	3380
ACTAGAAGTA GCCATGGGAC CACCTGTGGC CCAGAGGACT GCCTTTGTAC TTATGGTGGG	3440
GA CTGGGACC TGGGGATATA AGGGTCCAG GAGGACACTG CCAGGGGGCC AGTGCACTGC	3500
TCTGGGGAGA GGGGGCTCAG GAAGAGAGGA GGATAAGAAC AGTGAGAAGG AAGGATCCCT	3560
GGGTTGGGAG GCAGGCCCAG CATGGGTCAG CCATGCTTCC TCCTGGCTGT GTGACCCTGG	3620
GCAAGTCCCT TCCCCTCTCT GCGAAACAGT AGGGTGAGAC AATCCATTCT CTAAGACCCC	3680
TTTTAGATCC AAGTCCCCAT AGTTCTGTGG AGTCCCAGTA GAGGCCACCG AGGGTCCCTG	3740
CCCCCCTTGG GCACAGAGCT GACACTGAGT CCCTCAGTGG CCCCCTGAGT ATACCCCTT	3800
AGCCGGAGCC CCTTCCCCAT TCCTACAGCC AGAGGGGGAC CTGGCCTCAG CCTGGCAGGG	3860
CCTCTCTCCT CTTCAAGGCC ATATCCACCT GTGCCCCGGG GCTTGGGAGA CCCCCTAGGG	3920
CCGGAGCTCT GGGGTCATCC TGGCCACTGG CTTCTCCTTT CTCTGTTTTG TTCTGTATGT	3980
GTGTGGGGT GGGGGGAGGG GGGCCACCTG CTTACCTAT TCTGAGTTGC CTTAGAGAG	4040
ATGCGTTTTT TCTAGGACTC TGTGCAACTG TTGTATATGG TTCCGTGGGC TGACCGCTTT	4100
GTACATGAGA ATAAATCTAT TTCTTTCTAC C	4131

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 921 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Met	Arg	Arg	Gln	Pro	Ala	Ala	Ser	Arg	Asp	Leu	Phe	Ala	Gln	Glu	Pro
1				5					10					15	
Val	Pro	Pro	Gly	Ser	Gly	Asp	Gly	Ala	Leu	Gln	Asp	Ala	Leu	Leu	Ser
			20					25					30		
Leu	Gly	Ser	Val	Ile	Asp	Val	Ala	Gly	Leu	Gln	Gln	Ala	Val	Lys	Glu
		35					40					45			
Ala	Leu	Ser	Ala	Val	Leu	Pro	Lys	Val	Glu	Thr	Val	Tyr	Thr	Tyr	Leu
	50					55					60				

Leu Asp Gly Glu Ser Arg Leu Val Cys Glu Glu Pro Pro His Glu Leu
 65 70 75 80
 Pro Gln Glu Gly Lys Val Arg Glu Ala Val Ile Ser Arg Lys Arg Leu
 85 90 95
 Gly Cys Asn Gly Leu Gly Pro Ser Asp Leu Pro Gly Lys Pro Leu Ala
 100 105 110
 Arg Leu Val Ala Pro Leu Ala Pro Asp Thr Gln Val Leu Val Ile Pro
 115 120 125
 Leu Val Asp Lys Glu Ala Gly Ala Val Ala Ala Val Ile Leu Val His
 130 135 140
 Cys Gly Gln Leu Ser Asp Asn Glu Glu Trp Ser Leu Gln Ala Val Glu
 145 150 155 160
 Lys His Thr Leu Val Ala Leu Lys Arg Val Gln Ala Leu Gln Gln Arg
 165 170 175
 Glu Ser Ser Val Ala Pro Glu Ala Thr Gln Asn Pro Pro Glu Glu Ala
 180 185 190
 Ala Gly Asp Gln Lys Gly Gly Val Ala Tyr Thr Asn Gln Asp Arg Lys
 195 200 205
 Ile Leu Gln Leu Cys Gly Glu Leu Tyr Asp Leu Asp Ala Ser Ser Leu
 210 215 220
 Gln Leu Lys Val Leu Gln Tyr Leu Gln Gln Glu Thr Gln Ala Ser Arg
 225 230 235 240
 Cys Cys Leu Leu Leu Val Ser Glu Asp Asn Leu Gln Leu Ser Cys Lys
 245 250 255
 Val Ile Gly Asp Lys Val Leu Glu Glu Glu Ile Ser Phe Pro Leu Thr
 260 265 270
 Thr Gly Arg Leu Gly Gln Val Val Glu Asp Lys Lys Ser Ile Gln Leu
 275 280 285
 Lys Asp Leu Thr Ser Glu Asp Met Gln Gln Leu Gln Ser Met Leu Gly
 290 295 300
 Cys Glu Val Gln Ala Met Leu Cys Val Pro Val Ile Ser Arg Ala Thr
 305 310 315 320
 Asp Gln Val Val Ala Leu Ala Cys Ala Phe Asn Lys Leu Gly Gly Asp
 325 330 335
 Leu Phe Thr Asp Gln Asp Glu His Val Ile Gln His Cys Phe His Tyr
 340 345 350
 Thr Ser Thr Val Leu Thr Ser Thr Leu Ala Phe Gln Lys Glu Gln Lys
 355 360 365
 Leu Lys Cys Glu Cys Gln Ala Leu Leu Gln Val Ala Lys Asn Leu Phe
 370 375 380
 Thr His Leu Asp Asp Val Ser Val Leu Leu Gln Glu Ile Ile Thr Glu
 385 390 395 400
 Ala Arg Asn Leu Ser Asn Ala Glu Ile Cys Ser Val Phe Leu Leu Asp
 405 410 415

Gln Asn Glu Leu Val Ala Lys Val Phe Asp Gly Gly Val Val Glu Asp
420 425 430

Glu Ser Tyr Glu Ile Arg Il Pro Ala Asp Gln Gly Ile Ala Gly His
435 440 445

Val Ala Thr Thr Gly Gln Ile Leu Asn Ile Pro Asp Ala Tyr Ala His
450 455 460

Pro Leu Phe Tyr Arg Gly Val Asp Asp Ser Thr Gly Phe Arg Thr Arg
465 470 475 480

Asn Ile Leu Cys Phe Pro Ile Lys Asn Glu Asn Gln Glu Val Ile Gly
485 490 495

Val Ala Glu Leu Val Asn Lys Ile Asn Gly Pro Trp Phe Ser Lys Phe
500 505 510

Asp Glu Asp Leu Ala Thr Ala Phe Ser Ile Tyr Cys Gly Ile Ser Ile
515 520 525

Ala His Ser Leu Leu Tyr Lys Lys Val Asn Glu Ala Gln Tyr Arg Ser
530 535 540

His Leu Ala Asn Glu Met Met Met Tyr His Met Lys Val Ser Asp Asp
545 550 555 560

Glu Tyr Thr Lys Leu Leu His Asp Gly Ile Gln Pro Val Ala Ala Ile
565 570 575

Asp Ser Asn Phe Ala Ser Phe Thr Tyr Thr Pro Arg Ser Leu Pro Glu
580 585 590

Asp Asp Thr Ser Met Ala Ile Leu Ser Met Leu Gln Asp Met Asn Phe
595 600 605

Ile Asn Asn Tyr Lys Ile Asp Cys Pro Thr Leu Ala Arg Phe Cys Leu
610 615 620

Met Val Lys Lys Gly Tyr Arg Asp Pro Pro Tyr His Asn Trp Met His
625 630 635 640

Ala Phe Ser Val Ser His Phe Cys Tyr Leu Leu Tyr Lys Asn Leu Glu
645 650 655

Leu Thr Asn Tyr Leu Glu Asp Met Glu Ile Phe Ala Leu Phe Ile Ser
660 665 670

Cys Met Cys His Asp Leu Asp His Arg Gly Thr Asn Asn Ser Phe Gln
675 680 685

Val Ala Ser Lys Ser Val Leu Ala Ala Leu Tyr Ser Ser Glu Gly Ser
690 695 700

Val Met Glu Arg His His Phe Ala Gln Ala Ile Ala Ile Leu Asn Thr
705 710 715 720

His Gly Cys Asn Ile Phe Asp His Phe Ser Arg Lys Asp Tyr Gln Arg
725 730 735

Met Leu Asp Leu Met Arg Asp Ile Ile Leu Ala Thr Asp Leu Ala His
740 745 750

His Leu Arg Ile Phe Lys Asp Leu Gln Lys Met Ala Glu Val Gly Tyr
755 760 765

Asp Arg Thr Asn Lys Gln His His Ser Leu Leu Leu Cys Leu L u M t
 770 775 780

Thr Ser Cys Asp Leu Ser Asp Gln Thr Lys Gly Trp Lys Thr Thr Arg
 785 790 795 800

Lys Ile Ala Glu Leu Ile Tyr Lys Glu Phe Phe Ser Gln Gly Asp Leu
 805 810 815

Glu Lys Ala Met Gly Asn Arg Pro Met Glu Met Met Asp Arg Glu Lys
 820 825 830

Ala Tyr Ile Pro Glu Leu Gln Ile Ser Phe Met Glu His Ile Ala Met
 835 840 845

Pro Ile Tyr Lys Leu Leu Gln Asp Leu Phe Pro Lys Ala Ala Glu Leu
 850 855 860

Tyr Glu Arg Val Ala Ser Asn Arg Glu His Trp Thr Lys Val Ser His
 865 870 875 880

Lys Phe Thr Ile Arg Gly Leu Pro Ser Asn Asn Ser Leu Asp Phe Leu
 885 890 895

Asp Glu Glu Tyr Glu Val Pro Asp Leu Asp Gly Ala Arg Ala Pro Ile
 900 905 910

Asn Gly Cys Cys Ser Leu Asp Ala Glu
 915 920

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 249 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

ATATCGAATT CGGTTTAGTC TGGTTGGGA GGCAGACGAT GAGGAGCGAT GGGGCAGGCA	60
TGCGGCCACT CCATCCTCTG CAGGAGCCAG CAGTACCCGG CTGCGCGACC GGCTGAGCCG	120
CGGGGCCAGC AGGTCTTCCT CAAGCCGGAC GAGCCGCCGC CGCCGCCGCA GCCATGCGCC	180
GACAGCCTGC AGGATGCTTT GCTGAGCCTG GGCTCCGTCA TTGAGCTTGC AGGCTTGCGA	240
CAGGCTGTC	249

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 250 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GAATTCGGGT AGAGCAGGTA GCAGAAGTGG GAGACAGAAA AGGCGTGCAT CCAGTTGTGG	60
TAGGGGGGAT CCCGGTAGCC CTTCTTCACC ATCAAACAGA ACCGGGCCAG TGTCGGGCAG	120
TCAATTTTGT AGTTATTGAT GAAATTCATG TTCTGCAGCA TGCTCAGGAT GGCCATGGAG	180
TGTCATCCTT GGGCAGAGAG CGAGGAGTGT ATGTGAACTG GCAAGTTGGA GTCGATGGCA	240
GCCACAGGCT	250

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3789 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 181..3006

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CGCGGAACTG CCAGGGCAGC AGGGCTGGAT TGGGGTGTG AGTCCAGGCT GAGTCGGGGA	60
CAGGCCACTG TTCTTGGTCC CCGTGCCTGC TGGGCCAGGC GCCCTGCCTG GAGCCCCGGG	120
CAGGGTGAGC AGGGTGAGGT GCCACTTTAG TCTGGTTGGG GAGGCAGACG ATGAGGAGCG	180
ATG GGG CAG GCA TGC GGC CAC TCC ATC CTC TGC AGG AGC CAG CAG TAC Met Gly Gln Ala Cys Gly His Ser Ile Leu Cys Arg Ser Gln Gln Tyr	228
1 5 10 15	
CCG GCT GCG CGA CCG GCT GAG CCG CGG GGC CAG CAG GTC TTC CTC AAG	276
Pro Ala Ala Arg Pro Ala Glu Pro Arg Gly Gln Gln Val Phe Leu Lys	
20 25 30	
CCG GAC GAG CCG CCG CCG CCG CCG CAG CCA TGC GCC GAC AGC CTG CAG	324
Pro Asp Glu Pro Pro Pro Pro Pro Gln Pro Cys Ala Asp Ser Leu Gln	
35 40 45	
GAT GCT TTG CTG AGC CTG GGC TCC GTC ATT GAC GTT GCA GGC TTG CAA	372
Asp Ala Leu Leu Ser Leu Gly Ser Val Ile Asp Val Ala Gly Leu Gln	
50 55 60	
CAG GCT GTC AAG GAG GCC CTG TCG GCT GTG CTT CCC AAA GTG GAG ACG	420
Gln Ala Val Lys Glu Ala Leu Ser Ala Val Leu Pro Lys Val Glu Thr	
65 70 75 80	
GTC TAC ACC TAC CTG CTG GAT GGG GAA TCC CGG CTG GTG TGT GAG GAG	468
Val Tyr Thr Tyr Leu Leu Asp Gly Glu Ser Arg Leu Val Cys Glu Glu	
85 90 95	
CCC CCC CAC GAG CTG CCC CAG GAG GGG AAA GTG CGA GAG GCT GTG ATC	516
Pro Pro His Glu Leu Pro Gln Glu Lys Val Arg Glu Ala Val Ile	
100 105 110	
TCC CGG AAG CGG CTG GGC TGC AAT GGA CTG GGC CCC TCA GAC CTG CCT	564
Ser Arg Lys Arg Leu Gly Cys Asn Gly Leu Gly Pro Ser Asp Leu Pr	
115 120 125	

GGG Gly	AAG Lys	CCC Pro	TTG Leu	GCA Ala	AGG Arg	CTG Leu	GTG Val	GCT Ala	CCA Pro	CTG Leu	GCT Ala	CCT Pro	GAC Asp	ACC Thr	CAA Gln	612
130						135					140					
GTG Val	CTG Leu	GTC Val	ATA Ile	CCG Pro	CTG Leu	GTG Val	GAC Asp	AAG Lys	GAG Glu	GCC Ala	GGG Gly	GCT Ala	GTG Val	GCA Ala	GCT Ala	660
145					150					155					160	
GTC Val	ATC Ile	TTG Leu	GTG Val	CAC His	TGT Cys	GGT Gly	CAG Gln	CTG Leu	AGT Ser	GAC Asp	AAT Asn	GAG Glu	GAG Glu	TCG Trp	AGC Ser	708
				165					170						175	
CTG Leu	CAA Gln	GCT Ala	GTG Val	GAG Glu	AAG Lys	CAT His	ACC Thr	CTG Leu	GTG Val	GCC Ala	CTG Leu	AAA Lys	AGG Arg	GTG Val	CAG Gln	756
			180					185					190			
GCC Ala	TTG Leu	CAG Gln	CAG Gln	CGC Arg	GAG Glu	TCC Ser	AGC Ser	GTG Val	GCC Ala	CCG Pro	GAA Glu	GCG Ala	ACC Thr	CAG Gln	AAT Asn	804
		195					200					205				
CCT Pro	CCG Pro	GAG Glu	GAG Glu	GCA Ala	GCG Ala	GGA Gly	GAC Asp	CAG Gln	AAG Lys	GGT Gly	GGG Gly	GTC Val	GCA Ala	TAC Tyr	ACA Thr	852
	210					215					220					
GAC Asp	CAA Gln	GAC Asp	CGA Arg	AAG Lys	ATC Ile	CTG Leu	CAG Gln	CTT Leu	TGC Cys	GGG Gly	GAG Glu	CTC Leu	TAC Tyr	GAC Asp	CTG Leu	900
225					230					235					240	
GAT Asp	GCA Ala	TCT Ser	TCC Ser	CTG Leu	CAG Gln	CTC Leu	AAA Lys	GTG Val	CTC Leu	CAA Gln	TAT Tyr	CTG Leu	CAA Gln	CAG Gln	GAG Glu	948
				245				250						255		
ACC Thr	CAG Gln	GCA Ala	TCC Ser	CGC Arg	TGC Cys	TGC Cys	CTG Leu	CTG Leu	CTG Leu	GTA Val	TCC Ser	GAG Glu	GAC Asp	AAT Asn	CTT Leu	996
			260					265					270			
CAG Gln	CTC Leu	TCC Ser	TGC Cys	AAG Lys	GTC Val	ATT Ile	GGA Gly	GAT Asp	AAA Lys	GTA Val	CTG Leu	GAG Glu	GAA Glu	GAG Glu	ATC Ile	1044
		275					280					285				
AGC Ser	TTT Phe	CCG Pro	TTG Leu	ACC Thr	ACA Thr	GGA Gly	CGC Arg	CTG Leu	GGC Gly	CAA Gln	GTG Val	GTG Val	GAA Glu	GAC Asp	AAG Lys	1092
	290					295					300					
AAG Lys	TCT Ser	ATC Ile	CAG Gln	CTG Leu	AAA Lys	GAT Asp	CTC Leu	ACC Thr	TCC Ser	GAG Glu	GAT Asp	ATG Met	CAA Gln	CAG Gln	CTG Leu	1140
305					310					315					320	
CAA Gln	AGC Ser	ATG Met	TTG Leu	GCC Gly	TGT Cys	GAG Glu	GTG Val	CAG Gln	GCC Ala	ATG Met	CTC Leu	TGT Cys	GTC Val	CCT Pro	CTC Val	1188
				325					330					335		
ATC Ile	AGC Ser	CGG Arg	GCC Ala	ACT Thr	GAC Asp	CAG Gln	GTC Val	GTG Val	GCC Ala	CTG Leu	GCC Ala	TGT Cys	GCC Ala	TTC Phe	AAC Asn	1236
			340					345					350			
AAG Lys	CTC Leu	GGA Gly	GGA Gly	GAC Asp	TTG Leu	TTC Phe	ACA Thr	GAC Asp	CAG Gln	GAC Asp	GAG Glu	CAC His	GTG Val	ATC Ile	CAG Gln	1284
		355					360					365				
CAC His	TGC Cys	TTC Phe	CAC His	TAC Tyr	ACC Thr	AGC Ser	ACA Thr	GTG Val	CTC Leu	ACC Thr	AGC Ser	ACC Thr	CTG Leu	GCC Ala	TTC Phe	1332
	370					375					380					
CAG Gln	AAG Lys	GAG Glu	CAG Gln	AAG Lys	CTC Leu	AAG Lys	TGT Cys	GAG Glu	TGC Cys	CAG Gln	GCT Ala	CTT Leu	CTC Leu	CAA Gln	GTG Val	1380
385					390					395					400	

GCG Ala	AAG Lys	AAC Asn	CTC Leu	TTC Phe 405	ACT Thr	CAT His	CTG Leu	GAT Asp	GAC Asp 410	GTC Val	TCC Ser	GTG Val	CTG Leu	CTC Leu 415	CAG Gln	1428
GAG Glu	ATC Ile	ATC Ile	ACA Thr 420	GAG Glu	GCC Ala	AGG Arg	AAC Asn	CTC Leu 425	AGC Ser	AAT Asn	GCT Ala	GAG Glu	ATC Ile 430	TGC Cys	TCT Ser	1476
GTG Val	TTC Phe	CTG Leu 435	CTG Leu	GAT Asp	CAG Gln	AAC Asn	GAG Glu 440	CTG Leu	GTG Val	GCC Ala	AAG Lys	GTG Val 445	TTC Phe	GAT Asp	GGG Gly	1524
GGT Gly	GTG Val 450	GTG Val	GAA Glu	GAT Asp	GAG Glu	AGC Ser 455	TAT Tyr	GAG Glu	ATC Ile	CGC Arg	ATT Ile 460	CCC Pro	GCT Ala	GAC Asp	CAG Gln	1572
GGC Gly 465	ATC Ile	GCG Ala	GGT Gly	CAT His 470	GTG Val 470	GCG Ala	ACC Thr	ACC Thr	GGC Gly 475	CAG Gln 475	ATC Ile	CTA Leu	AAC Asn	ATC Ile	CCA Pro 480	1620
GAT Asp	GCT Ala	TAC Tyr	GCA Ala	CAT His 485	CCG Pro	CTT Leu	TTC Phe	TAC Tyr	CGA Arg 490	GGC Gly	GTG Val	GAC Asp	GAC Asp	AGC Ser 495	ACC Thr	1668
GGC Gly	TTC Phe	CGG Arg	ACG Thr 500	CGC Arg	AAC Asn	ATC Ile	CTC Leu	TGC Cys 505	TTC Phe	CCC Pro	ATC Ile	AAG Lys 510	AAC Asn 510	GAG Glu	AAC Asn	1716
CAG Gln	GAG Glu	GTC Val 515	ATC Ile	GGT Gly	GTG Val	GCC Ala	GAG Glu 520	CTG Leu	GTG Val	AAC Asn	AAG Lys 525	ATC Ile 525	AAT Asn	GGA Gly	CCA Pro	1764
TGG Trp	TTC Phe 530	AGC Ser	AAG Lys	TTT Phe	GAT Asp	GAA Glu 535	GAC Asp	CTG Leu	GCT Ala	ACA Thr	GCC Ala 540	TTC Phe	TCC Ser	ATC Ile	TAC Tyr	1812
TGT Cys 545	GGC Gly	ATC Ile	AGC Ser	ATT Ile	GCC Ala 550	CAT His	TCC Ser	CTC Leu	CTA Leu	TAC Tyr 555	AAG Lys	AAA Lys	GTG Val	AAT Asn	GAG Glu 560	1860
GCG Ala	CAG Gln	TAT Tyr	CGC Arg	AGC Ser 565	CAC His	CTT Leu	GCC Ala	AAT Asn	GAG Glu 570	ATG Met	ATG Met	ATG Met	TAC Tyr	CAC His 575	ATG Met	1908
AAG Lys	GTC Val	TCT Ser	GAT Asp 580	GAC Asp	GAG Glu	TAC Tyr	ACC Thr	AAA Lys 585	CTT Leu	CTC Leu	CAT His	GAC Asp	GGG Gly 590	ATC Ile	CAG Gln	1956
CCT Pro	GTG Val	GCT Ala 595	GCC Ala	ATC Ile	GAC Asp	TCC Ser	AAC Asn 600	TTT Phe	GCC Ala	AGT Ser	TTC Phe	ACA Thr 605	TAC Tyr	ACT Thr	CCT Pro	2004
CGC Arg	TCT Ser 610	CTG Leu	CCC Pro	GAG Glu	GAT Asp	GAC Asp 615	ACT Thr	TCC Ser	ATG Met	GCC Ala	ATC Ile 620	CTG Leu	AGC Ser	ATG Met	CTG Leu	2052
CAG Gln 625	GAC Asp	ATG Met	AAT Asn	TTC Phe 630	ATC Ile	AAT Asn	AAC Asn	TAC Tyr	AAA Lys 635	ATT Ile	GAC Asp	TGC Cys	CCG Pro	ACA Thr	CTG Leu 640	2100
GCC Ala	CGG Arg	TTC Phe	TGT Cys 645	TTG Leu	ATG Met	GTG Val	AAG Lys	AAG Lys	GGC Gly 650	TAC Tyr	CGG Arg	GAT Asp	CCC Pro	CCC Pro 655	TAC Tyr	2148
CAC His	AAC Asn	TGG Trp	ATG Met 660	CAC His	GCC Ala	TTT Phe	TCT Ser	GTC Val 665	TCC Ser	CAC His	TTC Phe	TGC Cys 670	TAC Tyr	CTG Leu	CTC Leu	2196

TAC AAG AAC CTG GAG CTC ACC AAC TAC CTC GAG GAC ATG GAG ATC TTT Tyr Lys Asn Leu Glu Leu Thr Asn Tyr Leu Glu Asp Met Glu Ile Ph 675 680 685	2244
GCC TTG TTT ATT TCC TGC ATG TGT CAC GAC CTG GAC CAC AGA GGC ACA Ala Leu Phe Ile Ser Cys Met Cys His Asp Leu Asp His Arg Gly Thr 690 695 700	2292
AAC AAC TCC TTC CAG GTG GCC TCG AAA TCT GTG CTG GCC GCG CTC TAC Asn Asn Ser Phe Gln Val Ala Ser Lys Ser Val Leu Ala Ala Leu Tyr 705 710 715 720	2340
AGC TCG GAA GGC TCT GTC ATG GAG AGG CAC CAC TTC GCT CAG GCC ATT Ser Ser Glu Gly Ser Val Met Glu Arg His His Phe Ala Gln Ala Ile 725 730 735	2388
GCC ATC CTC AAC ACC CAC GGC TGC AAC ATC TTT GAC CAC TTC TCC CGG Ala Ile Leu Asn Thr His Gly Cys Asn Ile Phe Asp His Phe Ser Arg 740 745 750	2436
AAG GAT TAT CAG CGC ATG TTG GAC CTG ATG CGG GAC ATC ATC TTG GCC Lys Asp Tyr Gln Arg Met Leu Asp Leu Met Arg Asp Ile Ile Leu Ala 755 760 765	2484
ACA GAT CTG GCC CAC CAC CTC CGC ATC TTC AAG GAC CTC CAA AAG ATG Thr Asp Leu Ala His His Leu Arg Ile Phe Lys Asp Leu Gln Lys Met 770 775 780	2532
GCC GAA GTG GGC TAT GAT CGA ACC AAC AAG CAG CAC CAC AGC CTC CTT Ala Glu Val Gly Tyr Asp Arg Thr Asn Lys Gln His His Ser Leu Leu 785 790 795 800	2580
CTC TGC CTC CTT ATG ACC TCC TGT GAC CTC TCT GAC CAG ACC AAG GGC Leu Cys Leu Leu Met Thr Ser Cys Asp Leu Ser Asp Gln Thr Lys Gly 805 810 815	2628
TGG AAG ACC ACG AGG AAG ATC GCG GAG CTG ATC TAC AAA GAG TTC TTC Trp Lys Thr Arg Lys Ile Ala Glu Leu Ile Tyr Lys Glu Phe Phe 820 825 830	2676
TCC CAG GGA GAC TTG GAG AAG GCC ATG GGC AAC AGG CCG ATG GAG ATG Ser Gln Gly Asp Leu Glu Lys Ala Met Gly Asn Arg Pro Met Glu Met 835 840 845	2724
ATG GAC CGT GAG AAG GCC TAC ATC CCC GAG CTG CAG ATC AGC TTC ATG Met Asp Arg Glu Lys Ala Tyr Pro Ile Glu Leu Gln Ile Ser Phe Met 850 855 860	2772
GAG CAC ATC GCA ATG CCC ATC TAC AAG CTG CTG CAA GAC CTG TTC CCC Glu His Ile Ala Met Pro Ile Tyr Lys Leu Leu Gln Asp Leu Phe Pro 865 870 875 880	2820
AAG GCG GCC GAG TTG TAC GAA CGC GTG GCC TCT AAT CGT GAG CAC TGG Lys Ala Ala Glu Leu Tyr Glu Arg Val Ala Ser Asn Arg Glu His Trp 885 890 895	2868
ACC AAG GTG TCA CAC AAG TTC ACC ATC CGA GGC CTC CCG AGC AAC AAC Thr Lys Val Ser His Lys Phe Thr Ile Arg Gly Leu Pro Ser Asn Asn 900 905 910	2916
TCG TTG GAC TTC CTG GAC GAG GAG TAT GAG GTG CCT GAC CTG GAT GGC Ser Leu Asp Phe Leu Asp Glu Glu Tyr Glu Val Pro Asp Leu Asp Gly 915 920 925	2964
GCT AGG GCT CCC ATC AAT GGC TGT TGC AGC CTT GAT GCT GAG Ala Arg Ala Pro Ile Asn Gly Cys Cys Ser Leu Asp Ala Glu 930 935 940	3006

TGAGTCCCTC CTGGGACCCC TCCCTGTCCA GGCCTCCTCC CACAAGCCTC CACGGGCCTG	3066
GCCGCACGCC CTGGGACCAG AGCCAAGGGT CCTGGATTCT AGGCCAGGAC TTCCCATGTG	3126
ACCCGGGCGA GGTCTGACCT TCCCGGGCCT CAGCTTTCTT GTCTGTATAA TGGAAGACTT	3186
CAGCCTCACT GAGACTTTGT CACTTGTCTT CTGAGAGCAC AGGGGTAACC AATGAGCAGT	3246
GGACCCTGCT CTGCACCTCT GACCGCATCT TGGCAAGTCC CCACCCTCCA GGCCACTCCT	3306
TCTCTGAGGC AGCCGGATGG TTTCTTCTGG GCCCCATTCC TGGCCTACCA GACCTGTGCC	3366
CTTTCCTGTG GGGGCACCCT CACTGGCTCC CAGGATCCTC AGGCAAGAAC ATGAGACATC	3426
TGAGTGGGCA AAGGGTGGGT CTTAGAGACA GTTATCAGCC TGGCTGGAGG ACTAGAAGTA	3486
GCCATGGGAC CACCTGTGGC CCAGAGGACT GCCTTTGTAC TTATGGTGGG GACTGGGACC	3546
TGGGGATATA AGGGTCCCAG GAGGACACTG CCAGGGGGCC AGTGCAGTGC TCTGGGGAGA	3606
GGGGGCTCAG GAAGAGAGGA GGATAAGAAC AGTGAGAAGG AAGGATCCCT GGGTTGGGAG	3666
GCAGGCCCAG CATGGGTCAG CCATGCTTCC TCCTGGCTGT GTGACCCTGG GCAAGTCCCT	3726
TCCCCTCTCT GCGAAACAGT AGGGTGAGAC AATCCATTCT CTAAGACCCC TTTTAGATCC	3786
AAG	3789

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 942 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Met	Gly	Gln	Ala	Cys	Gly	His	Ser	Ile	Leu	Cys	Arg	Ser	Gln	Gln	Tyr	1	5	10	15
Pro	Ala	Ala	Arg	Pro	Ala	Glu	Pro	Arg	Gly	Gln	Gln	Val	Phe	Leu	Lys	20	25	30	
Pro	Asp	Glu	Pro	Pro	Pro	Pro	Pro	Gln	Pro	Cys	Ala	Asp	Ser	Leu	Gln	35	40	45	
Asp	Ala	Leu	Leu	Ser	Leu	Gly	Ser	Val	Ile	Asp	Val	Ala	Gly	Leu	Gln	50	55	60	
Gln	Ala	Val	Lys	Glu	Ala	Leu	Ser	Ala	Val	Leu	Pro	Lys	Val	Glu	Thr	65	70	75	80
Val	Tyr	Thr	Tyr	Leu	Leu	Asp	Gly	Glu	Ser	Arg	Leu	Val	Cys	Glu	Glu	85	90	95	
Pro	Pro	His	Glu	Leu	Pro	Gln	Glu	Gly	Lys	Val	Arg	Glu	Ala	Val	Ile	100	105	110	
Ser	Arg	Lys	Arg	Leu	Gly	Cys	Asn	Gly	Leu	Gly	Pro	Ser	Asp	Leu	Pro	115	120	125	
Gly	Lys	Pro	Leu	Ala	Arg	Leu	Val	Ala	Pro	Leu	Ala	Pro	Asp	Thr	Gln	130	135	140	

Val Leu Val Ile Pro Leu Val Asp Lys Glu Ala Gly Ala Val Ala Ala
145 150 155 160

Val Il Leu Val His Cys Gly Gln Leu Ser Asp Asn Glu Glu Trp Ser
165 170 175

Leu Gln Ala Val Glu Lys His Thr Leu Val Ala Leu Lys Arg Val Gln
180 185 190

Ala Leu Gln Gln Arg Glu Ser Ser Val Ala Pro Glu Ala Thr Gln Asn
195 200 205

Pro Pro Glu Glu Ala Ala Gly Asp Gln Lys Gly Gly Val Ala Tyr Thr
210 215 220

Asp Gln Asp Arg Lys Ile Leu Gln Leu Cys Gly Glu Leu Tyr Asp Leu
225 230 235 240

Asp Ala Ser Ser Leu Gln Leu Lys Val Leu Gln Tyr Leu Gln Gln Glu
245 250 255

Thr Gln Ala Ser Arg Cys Cys Leu Leu Leu Val Ser Glu Asp Asn Leu
260 265 270

Gln Leu Ser Cys Lys Val Ile Gly Asp Lys Val Leu Glu Glu Glu Ile
275 280 285

Ser Phe Pro Leu Thr Thr Gly Arg Leu Gly Gln Val Val Glu Asp Lys
290 295 300

Lys Ser Ile Gln Leu Lys Asp Leu Thr Ser Glu Asp Met Gln Gln Leu
305 310 315 320

Gln Ser Met Leu Gly Cys Glu Val Gln Ala Met Leu Cys Val Pro Val
325 330 335

Ile Ser Arg Ala Thr Asp Gln Val Val Ala Leu Ala Cys Ala Phe Asn
340 345 350

Lys Leu Gly Gly Asp Leu Phe Thr Asp Gln Asp Glu His Val Ile Gln
355 360 365

His Cys Phe His Tyr Thr Ser Thr Val Leu Thr Ser Thr Leu Ala Phe
370 375 380

Gln Lys Glu Gln Lys Leu Lys Cys Glu Cys Gln Ala Leu Leu Gln Val
385 390 395 400

Ala Lys Asn Leu Phe Thr His Leu Asp Asp Val Ser Val Leu Leu Gln
405 410 415

Glu Ile Ile Thr Glu Ala Arg Asn Leu Ser Asn Ala Glu Ile Cys Ser
420 425 430

Val Phe Leu Leu Asp Gln Asn Glu Leu Val Ala Lys Val Phe Asp Gly
435 440 445

Gly Val Val Glu Asp Glu Ser Tyr Glu Ile Arg Ile Pro Ala Asp Gln
450 455 460

Gly Ile Ala Gly His Val Ala Thr Thr Gly Gln Ile Leu Asn Ile Pro
465 470 475 480

Asp Ala Tyr Ala His Pro Leu Phe Tyr Arg Gly Val Asp Asp Ser Thr
485 490 495

Gly Phe Arg Thr Arg Asn Ile Leu Cys Phe Pro Ile Lys Asn Glu Asn
500 505 510

Gln Glu Val Ile Gly Val Ala Glu Leu Val Asn Lys Ile Asn Gly Pro
515 520 525

Trp Phe Ser Lys Phe Asp Glu Asp Leu Ala Thr Ala Phe Ser Ile Tyr
530 535 540

Cys Gly Ile Ser Ile Ala His Ser Leu Leu Tyr Lys Lys Val Asn Glu
545 550 555 560

Ala Gln Tyr Arg Ser His Leu Ala Asn Glu Met Met Met Tyr His Met
565 570 575

Lys Val Ser Asp Asp Glu Tyr Thr Lys Leu Leu His Asp Gly Ile Gln
580 585 590

Pro Val Ala Ala Ile Asp Ser Asn Phe Ala Ser Phe Thr Tyr Thr Pro
595 600 605

Arg Ser Leu Pro Glu Asp Asp Thr Ser Met Ala Ile Leu Ser Met Leu
610 615 620

Gln Asp Met Asn Phe Ile Asn Asn Tyr Lys Ile Asp Cys Pro Thr Leu
625 630 635 640

Ala Arg Phe Cys Leu Met Val Lys Lys Gly Tyr Arg Asp Pro Pro Tyr
645 650 655

His Asn Trp Met His Ala Phe Ser Val Ser His Phe Cys Tyr Leu Leu
660 665 670

Tyr Lys Asn Leu Glu Leu Thr Asn Tyr Leu Glu Asp Met Glu Ile Phe
675 680 685

Ala Leu Phe Ile Ser Cys Met Cys His Asp Leu Asp His Arg Gly Thr
690 695 700

Asn Asn Ser Phe Gln Val Ala Ser Lys Ser Val Leu Ala Ala Leu Tyr
705 710 715 720

Ser Ser Glu Gly Ser Val Met Glu Arg His His Phe Ala Gln Ala Ile
725 730 735

Ala Ile Leu Asn Thr His Gly Cys Asn Ile Phe Asp His Phe Ser Arg
740 745 750

Lys Asp Tyr Gln Arg Met Leu Asp Leu Met Arg Asp Ile Ile Leu Ala
755 760 765

Thr Asp Leu Ala His His Leu Arg Ile Phe Lys Asp Leu Gln Lys Met
770 775 780

Ala Glu Val Gly Tyr Asp Arg Thr Asn Lys Gln His His Ser Leu Leu
785 790 795 800

Leu Cys Leu Leu Met Thr Ser Cys Asp Leu Ser Asp Gln Thr Lys Gly
805 810 815

Trp Lys Thr Thr Arg Lys Ile Ala Glu Leu Ile Tyr Lys Glu Phe Phe
820 825 830

Ser Gln Gly Asp Leu Glu Lys Ala Met Gly Asn Arg Pro Met Glu Met
835 840 845

Met Asp Arg Glu Lys Ala Tyr Ile Pro Glu Leu Gln Ile Ser Phe Met
 850 855 860

Glu His Ile Ala Met Pro Ile Tyr Lys Leu Leu Gln Asp Leu Phe Pro
 865 870 875 880

Lys Ala Ala Glu Leu Tyr Glu Arg Val Ala Ser Asn Arg Glu His Trp
 885 890 895

Thr Lys Val Ser His Lys Phe Thr Ile Arg Gly Leu Pro Ser Asn Asn
 900 905 910

Ser Leu Asp Phe Leu Asp Glu Glu Tyr Glu Val Pro Asp Leu Asp Gly
 915 920 925

Ala Arg Ala Pro Ile Asn Gly Cys Cys Ser Leu Asp Ala Glu
 930 935 940

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3044 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 12..2834

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GAATTCTGAT A ATG GGG CAG GCA TGC GGC CAC TCC ATC CTC TGC AGG AGC	50
Met Gly Gln Ala Cys Gly His Ser Ile Leu Cys Arg Ser	
1 5 10	
CAG CAG TAC CCG GCA GCG CGA CCG GCT GAG CCG CGG GGC CAG CAG GTC	98
Gln Gln Tyr Pro Ala Ala Arg Pro Ala Glu Pro Arg Gly Gln Gln Val	
15 20 25	
TTC CTC AAG CCG GAC GAG CCG CCG CCG CCG CCG CAG CCA TGC GCC GAC	146
Phe Leu Lys Pro Asp Glu Pro Pro Pro Pro Pro Gln Pro Cys Ala Asp	
30 35 40 45	
AGC CTG CAG GAC GCC TTG CTG AGT CTG GGC TCT GTC ATC GAC ATT TCA	194
Ser Leu Gln Asp Ala Leu Leu Ser Leu Gly Ser Val Ile Asp Ile Ser	
50 55 60	
GGC CTG CAA CGT GCT GTC AAG GAG GCC CTG TCA GCT GTG CTC CCC CGA	242
Gly Leu Gln Arg Ala Val Lys Glu Ala Leu Ser Ala Val Leu Pro Arg	
65 70 75	
GTG GAA ACT GTC TAC ACC TAC CTA CTG GAT GGT GAG TCC CAG CTG GTG	290
Val Glu Thr Val Tyr Thr Tyr Leu Leu Asp Gly Glu Ser Gln Leu Val	
80 85 90	
TGT GAG GAC CCC CCA CAT GAG CTG CCC CAG GAG GGG AAA GTC CGG GAG	338
Cys Glu Asp Pro Pro His Glu Leu Pro Gln Glu Gly Lys Val Arg Glu	
95 100 105	
GCT ATC ATC TCC CAG AAG CGG CTG GGC TGC AAT GGG CTG GGC TTC TCA	386
Ala Ile Ile Ser Gln Lys Arg Leu Gly Cys Asn Gly Leu Gly Phe Ser	
110 115 120 125	

GAC CTG CCA GGG AAG CCC TTG GCC AGG CTG GTG GCT CCA CTG GCT CCT Asp Leu Pro Gly Lys Pro Leu Ala Arg Leu Val Ala Pro Leu Ala Pro	434
GAT ACC CAA GTG CTG GTC ATG CCG CTA GCG GAC AAG GAG GCT GGG GCC Asp Thr Gln Val Leu Val Met Pro Leu Ala Asp Lys Glu Ala Gly Ala	532
GTG GCA GCT GTC ATC TTG GTG CAC TGT GGC CAG CTG AGT GAT AA. GAG Val Ala Ala Val Ile Leu Val His Cys Gly Gln Leu Ser Asp Asn Glu	530
GAA TGG AGC CTG CAG GCG GTG GAG AAG CAT ACC CTG GTC GCC CTG CGG Glu Trp Ser Leu Gln Ala Val Glu Lys His Thr Leu Val Ala Leu Arg	578
AGG GTG CAG GTC CTG CAG CAG CGC GGG CCC AGG GAG GCT CCC CGA GCC Arg Val Gln Val Leu Gln Gln Arg Gly Pro Arg Glu Ala Pro Arg Ala	626
GTC CAG AAC CCC CCG GAG GGG ACG GCG GAA GAC CAG AAG GGC GGG GCG Val Gln Asn Pro Pro Glu Gly Thr Ala Glu Asp Gln Lys Gly Gly Ala	674
GCG TAC ACC GAC CGC GAC CGC AAG ATC CTC CAA CTG TGC GGG GAA CTC Ala Tyr Thr Asp Arg Asp Arg Lys Ile Leu Gln Leu Cys Gly Glu Leu	722
TAC GAC CTG GAT GCC TCT TCC CTG CAG CTC AAA GTG CTC CAA TAC CTG Tyr Asp Leu Asp Ala Ser Ser Leu Gln Leu Lys Val Leu Gln Tyr Leu	770
CAG CAG GAG ACC CGG GCA TCC CGC TGC TGC CTC CTG CTG GTG TCG GAG Gln Gln Glu Thr Arg Ala Ser Arg Cys Cys Leu Leu Val Ser Glu	818
GAC AAT CTC CAG CTT TCT TGC AAG GTC ATC GGA GAC AAA GTG CTC GGG Asp Asn Leu Gln Leu Ser Cys Lys Val Ile Glu Asp Lys Val Leu Gly	866
GAA GAG GTC AGC TTT CCC TTG ACA GGA TGC CTG GGC CAG GTG GTG GAA Glu Glu Val Ser Phe Pro Leu Thr Gly Cys Leu Gly Gln Val Val Glu	914
GAC AAG AAG TCC ATC CAG CTG AAG GAC CTC ACC TCC GAG GAT GTA CAA Asp Lys Lys Ser Ile Gln Leu Lys Asp Leu Thr Ser Glu Asp Val Gln	962
CAG CTG CAG AGC ATG TTG GGC TGT GAG CTG CAG GCC ATG CTC TGT GTC Gln Leu Gln Ser Met Leu Gly Cys Glu Leu Gln Ala Met Leu Cys Val	1010
CCT GTC ATC AGC CGG GCC ACT GAC CAG GTG GTG GCC TTG GCC TGC GCC Pro Val Ile Ser Arg Ala Thr Asp Gln Val Val Ala Leu Ala Cys Ala	1058
TTC AAC AAG CTA GAA GGA GAC TTG TTC ACC GAC GAG GAC GAG CAT GTG Phe Asn Lys Leu Glu Gly Asp Leu Phe Thr Asp Glu Asp Glu His Val	1106
ATC CAG CAC TGC TTC CAC TAC ACC AGC ACC GTG CTC ACC AGC ACC CTG Ile Gln His Cys Phe His Tyr Thr Ser Thr Val Leu Thr Ser Thr Leu	1154
GCC TTC CAG AAG GAA CAG AAA CTC AAG TGT GAG TGC CAG GCT CTT CTC Ala Phe Gln Lys Glu Gln Lys Leu Lys Cys Glu Cys Gln Ala Leu Leu	1202

CAA	GTG	GCA	AAG	AAC	CTC	TTC	ACC	CAC	CTG	GAT	GAC	GTC	TCT	GTC	CTG	1250
Gln	Val	Ala	Lys	Asn	Leu	Phe	Thr	His	Leu	Asp	Asp	Val	Ser	Val	Leu	
		400					405					410				
CTC	CAG	GAG	ATC	ATC	ACG	GAG	GCC	AGA	AAC	CTC	AGC	AAC	GCA	GAG	ATC	1298
Leu	Gln	Glu	Ile	Ile	Thr	Glu	Ala	Arg	Asn	Leu	Ser	Asn	Ala	Glu	Ile	
	415					420					425					
TGC	TCT	GTG	TTC	CTG	CTG	GAT	CAG	AAT	GAG	CTG	GTG	GCC	AAG	GTG	TTC	1346
Cys	Ser	Val	Phe	Leu	Leu	Asp	Gln	Asn	Glu	Leu	Val	GCC	Ala	Lys	Val	
430					435					440					445	
GAC	GGG	GGC	GTG	GTG	GAT	GAT	GAG	AGC	TAT	GAG	ATC	CGC	ATC	CCG	GCC	1394
Asp	Gly	Gly	Val	Val	Asp	Asp	Glu	Ser	Tyr	Glu	Ile	Arg	Ile	Pro	Ala	
				450					455					460		
GAT	CAG	GGC	ATC	GCG	GGA	CAC	GTG	GCG	ACC	ACG	GGC	CAG	ATC	CTG	AAC	1442
Asp	Gln	Gly	Ile	Ala	Gly	His	Val	Ala	Thr	Thr	Gly	Gln	Ile	Leu	Asn	
			465				470						475			
ATC	CCT	GAC	GCA	TAT	GCC	CAT	CCG	CTT	TTC	TAC	CGC	GGC	GTG	GAC	GAC	1490
Ile	Pro	Asp	Ala	Tyr	Ala	His	Pro	Leu	Phe	Tyr	Arg	Gly	Val	Asp	Asp	
		480					485					490				
AGC	ACC	GGC	TTC	CGC	ACG	CGC	AAC	ATC	CTC	TGC	TTC	CCC	ATC	AAG	AAC	1538
Ser	Thr	Gly	Phe	Arg	Thr	Arg	Asn	Ile	Leu	Cys	Phe	Pro	Ile	Lys	Asn	
	495					500					505					
GAG	AAC	CAG	GAG	GTC	ATC	GGT	GTG	JCC	GAG	CTG	GTG	AAC	AAG	ATC	AAT	1586
Glu	Asn	Gln	Glu	Val	Ile	Gly	Val	Ala	Glu	Leu	Val	Asn	Lys	Ile	Asn	
510					515					520					525	
GGG	CCA	TGG	TTC	AGC	AAG	TTC	GAC	GAG	GAC	CTG	GCG	ACG	GCC	TTC	TCC	1634
Gly	Pro	Trp	Phe	Ser	Lys	Phe	Asp	Glu	Asp	Leu	Ala	Thr	Ala	Phe	Ser	
				530					535					540		
ATC	TAC	TGC	GGC	ATC	AGC	ATC	GCC	CAT	TCT	CTC	CTA	TAC	AAA	AAA	GTG	1682
Ile	Tyr	Cys	Gly	Ile	Ser	Ile	Ala	His	Ser	Leu	Leu	Tyr	Lys	Lys	Val	
			545				550						555			
AAT	GAG	GCT	CAG	TAT	CGC	AGC	CAC	CTG	GCC	AAT	GAG	ATG	ATG	ATG	TAC	1730
Asn	Gln	Ala	Gln	Tyr	Arg	Ser	His	Leu	Ala	Asn	Glu	Met	Met	Met	Tyr	
		560					565					570				
CAC	ATG	AAG	GTC	TCC	GAC	GAT	GAG	TAT	ACC	AAA	CTT	CTC	CAT	GAT	GGG	1778
His	Met	Lys	Val	Ser	Asp	Asp	Glu	Tyr	Thr	Lys	Leu	Leu	His	Asp	Gly	
		575				580					585					
ATC	CAG	CCT	GTG	GCT	GCC	ATT	GAC	TCC	AAT	TTT	GCA	AGT	TTC	ACC	TAT	1826
Ile	Gln	Pro	Val	Ala	Ala	Ile	Asp	Ser	Asn	Phe	Ala	Ser	Phe	Thr	Tyr	
590					595					600					605	
ACC	CCT	CGT	TCC	CTG	CCC	GAG	GAT	GAC	ACG	TCC	ATG	GCC	ATC	CTG	AGC	1874
Thr	Pro	Arg	Ser	Leu	Pro	Glu	Asp	Asp	Thr	Ser	Met	Ala	Ile	Leu	Ser	
				610					615					620		
ATG	CTG	CAG	GAC	ATG	AAT	TTC	ATC	AAC	AAC	TAC	AAA	ATT	GAC	TGC	CCG	1922
Met	Leu	Gln	Asp	Met	Asn	Phe	Ile	Asn	Asn	Tyr	Lys	Ile	Asp	Cys	Pro	
			625				630						635			
ACC	CTG	GCC	CGG	TTC	TGT	TTG	ATG	GTG	AAG	AAG	GGC	TAC	CGG	GAT	CCC	1970
Thr	Leu	Ala	Arg	Phe	Cys	Leu	Met	Val	Lys	Lys	Gly	Tyr	Arg	Asp	Pro	
		640				645						650				
CCC	TAC	CAC	AAC	TGG	ATG	CAC	GCC	TTT	TCT	GTC	TCC	CAC	TTC	TGC	TAC	2018
Pro	Tyr	His	Asn	Trp	Met	His	Ala	Phe	Ser	Val	Ser	His	Phe	Cys	Tyr	
	655					660					665					

CTG Leu 670	CTC Leu	TAC Tyr	AAG Lys	AAC Asn	CTG Leu 675	GAG Glu	CTC Leu	ACC Thr	AAC Asn	TAC Tyr 680	CTC Leu	GAG Glu	GAC Asp	ATC Ile	GAG Glu 685	2066
ATC Ile	TTT Phe	GCC Ala	TTG Leu	TTT Phe 690	ATT Ile	TCC Ser	TGC Cys	ATG Met	TGT Cys 695	CAT His	GAC Asp	CTG Leu	GAC Asp	CAC His	AGA Arg 700	2114
GGC Gly	ACA Thr	AAC Asn	AAC Asn 705	TCT Ser	TTC Phe	CAG Gln	GTG Val	GCC Ala 710	TCG Ser	AAA Lys	TCT Ser	GTG Val	CTG Leu 715	GCT Ala	GCG Ala	2162
CTC Leu	TAC Tyr	AGC Ser 720	TCT Ser	GAG Glu	GGC Gly	TCC Ser	GTG Val 725	ATG Met	GAG Glu	AGG Arg	CAC His	CAC His	TTT Phe	GCT Ala	CAG Gln	2210
GCC Ala 735	ATC Ile	GCC Ala	ATC Ile	CTC Leu	AAC Asn	ACC Thr 740	CAC His	GGC Gly	TGC Cys	AAC Asn	ATC Ile 745	TTT Phe	GAT Asp	CAT His	TTC Phe	2258
TCC Ser 750	CGG Arg	AAG Lys	GAC Asp	TAT Tyr	CAG Gln 755	CGC Arg	ATG Met	CTG Leu	GAT Asp	CTG Leu 760	ATG Met	CGG Arg	GAC Asp	ATC Ile	ATC Ile 765	2306
TTG Leu	GCC Ala	ACA Thr	GAC Asp	CTG Leu 770	GCC Ala	CAC His	CAT His	CTC Leu	CGC Arg 775	ATC Ile	TTC Phe	AAG Lys	GAC Asp	CTC Leu 780	CAG Gln	2354
AAG Lys	ATG Met	GCT Ala	GAG Glu 785	GTG Val	GGC Gly	TAC Tyr	GAC Asp 790	CGA Arg	AAC Asn	AAC Asn	AAG Lys	CAG Gln	CAC His	CAC His	AGA Arg	2402
CTT Leu	CTC Leu	CTC Leu 800	TGC Cys	CTC Leu	CTC Leu	ATG Met	ACC Thr 805	TCC Ser	TGT Cys	GAC Asp	CTC Leu	TCT Ser	GAC Asp	CAG Gln	ACC Thr	2450
AAG Lys 815	GGC Gly	TGG Trp	AAG Lys	ACT Thr	ACG Thr	AGA Arg 820	AAG Lys	ATC Ile	CGC Ala	GAG Glu	CTG Leu 825	ATC Ile	TAC Tyr	AAA Lys	GAA Glu	2498
TTC Phe 830	TTC Phe	TCC Ser	CAG Gln	GGA Gly	GAC Asp 835	CTG Leu	GAG Glu	AAG Lys	GCC Ala	ATG Met 840	GGC Gly	AAC Asn	AGG Arg	CCG Pro	ATG Met 845	2546
GAG Glu	ATG Met	ATG Met	GAC Asp	CGG Arg 850	GAG Glu	AAG Lys	GCC Ala	TAT Tyr	ATC Ile 855	CCT Pro	GAG Glu	CTG Leu	CAA Gln	ATC Ile	AGC Ser 860	2594
TTC Phe	ATG Met	GAG Glu	CAC His 865	ATT Ile	GCA Ala	ATG Met	CCC Pro	ATC Ile 870	TAC Tyr	AAG Lys	CTG Leu	TTG Leu	CAG Gln	GAC Asp	CTG Leu	2642
TTC Phe	CCC Pro	AAA Lys 880	GCG Ala	GCA Ala	GAG Glu	CTG Leu	TAC Tyr 885	GAG Glu	CGC Arg	GTG Val	GCC Ala	TCC Ser	AAC Asn	CGT Arg	GAG Glu	2690
CAC His	TGG Trp 895	ACC Thr	AAG Lys	GTG Val	TCC Ser	CAC His 900	AAG Lys	TTC Phe	ACC Thr	ATC Ile	CGC Arg 905	GGC Gly	CTC Leu	CCA Pro	AGT Ser	2738
AAC Asn 910	AAC Asn	TCG Ser	CTG Leu	GAC Asp	TTC Phe 915	CTG Leu	GAT Asp	GAG Glu	GAG Glu	TAC Tyr 920	GAG Glu	GTG Val	CCT Pro	GAT Asp	CTG Leu 925	2786
GAT Asp	GGC Gly	ACT Thr	AGG Arg	GCC Ala 930	CCC Pro	ATC Ile	AAT Asn	GGC Gly	TGC Cys 935	TGC Cys	AGC Ser	CTT Leu	GAT Asp	GCT Ala	GAG Glu 940	2834

TGACTCGAGC GTCATATTAA TGGACGCAAA GCAAGGAAAT TCGAGCGGG AAATAAGAAA	2894
CGATAGAAGT AGGAATCGAT ACCCGGTGCG TGCACATAAC AGTCTTTTAC CAATTAACAG	2954
GAGAGATTGA AGTGTGCGAGA TACGAAATGA AATTTACTAC GACTACCGTA AAGAAATGCA	3014
TAAGCTCTGT TAGAGAAAAA TTGGTAGCCA	3044

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 941 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Met	Gly	Gln	Ala	Cys	Gly	His	Ser	Ile	Leu	Cys	Arg	Ser	Gln	Gln	Tyr	1	5	10	15
Pro	Ala	Ala	Arg	Pro	Ala	Glu	Pro	Arg	Gly	Gln	Gln	Val	Phe	Leu	Lys	20	25	30	
Pro	Asp	Glu	Pro	Pro	Pro	Pro	Pro	Gln	Pro	Cys	Ala	Asp	Ser	Leu	Gln	35	40	45	
Asp	Ala	Leu	Leu	Ser	Leu	Gly	Ser	Val	Ile	Asp	Ile	Ser	Gly	Leu	Gln	50	55	60	
Arg	Ala	Val	Lys	Glu	Ala	Leu	Ser	Ala	Val	Leu	Pro	Arg	Val	Glu	Thr	65	70	75	80
Val	Tyr	Thr	Tyr	Leu	Asp	Gly	Glu	Ser	Gln	Leu	Val	Cys	Glu	Asp		85	90	95	
Pro	Pro	His	Glu	Leu	Pro	Gln	Glu	Gly	Lys	Val	Arg	Glu	Ala	Ile	Ile	100	105	110	
Ser	Gln	Lys	Arg	Leu	Gly	Cys	Asn	Gly	Leu	Gly	Phe	Ser	Asp	Leu	Pro	115	120	125	
Gly	Lys	Pro	Leu	Ala	Arg	Leu	Val	Ala	Pro	Leu	Ala	Pro	Asp	Thr	Gln	130	135	140	
Val	Leu	Val	Met	Pro	Leu	Ala	Asp	Lys	Glu	Ala	Gly	Ala	Val	Ala	Ala	145	150	155	160
Val	Ile	Leu	Val	His	Cys	Gly	Gln	Leu	Ser	Asp	Asn	Glu	Glu	Trp	Ser	165	170	175	
Leu	Gln	Ala	Val	Glu	Lys	His	Thr	Leu	Val	Ala	Leu	Arg	Arg	Val	Gln	180	185	190	
Val	Leu	Gln	Gln	Arg	Gly	Pro	Arg	Glu	Ala	Pro	Arg	Ala	Val	Gln	Asn	195	200	205	
Pro	Pro	Glu	Gly	Thr	Ala	Glu	Asp	Gln	Lys	Gly	Gly	Ala	Ala	Tyr	Thr	210	215	220	
Asp	Arg	Asp	Arg	Lys	Ile	Leu	Gln	Leu	Cys	Gly	Glu	Leu	Tyr	Asp	Leu	225	230	235	240
Asp	Ala	Ser	Ser	Leu	Gln	Leu	Lys	Val	Leu	Gln	Tyr	Leu	Gln	Gln	Glu	245	250	255	

Thr Arg Ala Ser Arg Cys Cys Leu Leu Leu Val Ser Glu Asp Asn Leu
 260 265 270
 Gln Leu Ser Cys Lys Val Ile Gly Asp Lys Val Leu Gly Glu Glu Val
 275 280 285
 Ser Phe Pro Leu Thr Gly Cys Leu Gly Gln Val Val Glu Asp Lys Lys
 290 295 300
 Ser Ile Gln Leu Lys Asp Leu Thr Ser Glu Asp Val Gln Gln Leu Gln
 305 310 315 320
 Ser Met Leu Gly Cys Glu Leu Gln Ala Met Leu Cys Val Pro Val Ile
 325 330 335
 Ser Arg Ala Thr Asp Gln Val Val Ala Leu Ala Cys Ala Phe Asn Lys
 340 345 350
 Leu Glu Gly Asp Leu Phe Thr Asp Glu Asp Glu His Val Ile Gln His
 355 360 365
 Cys Phe His Tyr Thr Ser Thr Val Leu Thr Ser Thr Leu Ala Phe Gln
 370 375 380
 Lys Glu Gln Lys Leu Lys Cys Glu Cys Gln Ala Leu Leu Gln Val Ala
 385 390 395 400
 Lys Asn Leu Phe Thr His Leu Asp Asp Val Ser Val Leu Leu Gln Glu
 405 410 415
 Ile Ile Thr Glu Ala Arg Asn Leu Ser Asn Ala Glu Ile Cys Ser Val
 420 425 430
 Phe Leu Leu Asp Gln Asn Glu Leu Val Ala Lys Val Phe Asp Gly Gly
 435 440 445
 Val Val Asp Asp Glu Ser Tyr Glu Ile Arg Ile Pro Ala Asp Gln Gly
 450 455 460
 Ile Ala Gly His Val Ala Thr Thr Gly Gln Ile Leu Asn Ile Pro Asp
 465 470 475 480
 Ala Tyr Ala His Pro Leu Phe Tyr Arg Gly Val Asp Asp Ser Thr Gly
 485 490 495
 Phe Arg Thr Arg Asn Ile Leu Cys Phe Pro Ile Lys Asn Glu Asn Gln
 500 505 510
 Glu Val Ile Gly Val Ala Glu Leu Val Asn Lys Ile Asn Gly Pro Trp
 515 520 525
 Phe Ser Lys Phe Asp Glu Asp Leu Ala Thr Ala Phe Ser Ile Tyr Cys
 530 535 540
 Gly Ile Ser Ile Ala His Ser Leu Leu Tyr Lys Lys Val Asn Glu Ala
 545 550 555 560
 Gln Tyr Arg Ser His Leu Ala Asn Glu Met Met Met Tyr His Met Lys
 565 570 575
 Val Ser Asp Asp Glu Tyr Thr Lys Leu Leu His Asp Gly Ile Gln Pro
 580 585 590
 Val Ala Ala Ile Asp Ser Asn Phe Ala Ser Phe Thr Tyr Thr Pro Arg
 595 600 605

Ser Leu Pro Glu Asp Asp Thr Ser Met Ala Ile Leu Ser Met Leu Gln
610 615 620

Asp Met Asn Phe Ile Asn Asn Tyr Lys Ile Asp Cys Pro Thr Leu Ala
625 630 635 640

Arg Phe Cys Leu Met Val Lys Lys Gly Tyr Arg Asp Pro Pro Tyr His
645 650 655

Asn Trp Met His Ala Phe Ser Val Ser His Phe Cys Tyr Leu Leu Tyr
660 665 670

Lys Asn Leu Glu Leu Thr Asn Tyr Leu Glu Asp Ile Glu Ile Phe Ala
675 680 685

Leu Phe Ile Ser Cys Met Cys His Asp Leu Asp His Arg Gly Thr Asn
690 695 700

Asn Ser Phe Gln Val Ala Ser Lys Ser Val Leu Ala Ala Leu Tyr Ser
705 710 715 720

Ser Glu Gly Ser Val Met Glu Arg His His Phe Ala Gln Ala Ile Ala
725 730 735

Ile Leu Asn Thr His Gly Cys Asn Ile Phe Asp His Phe Ser Arg Lys
740 745 750

Asp Tyr Gln Arg Met Leu Asp Leu Met Arg Asp Ile Ile Leu Ala Thr
755 760 765

Asp Leu Ala His His Leu Arg Ile Phe Lys Asp Leu Gln Lys Met Ala
770 775 780

Glu Val Gly Tyr Asp Arg Asn Asn Lys Gln His His Arg Leu Leu Leu
785 790 795 800

Cys Leu Leu Met Thr Ser Cys Asp Leu Ser Asp Gln Thr Lys Gly Trp
805 810 815

Lys Thr Thr Arg Lys Ile Ala Glu Leu Ile Tyr Lys Glu Phe Phe Ser
820 825 830

Gln Gly Asp Leu Glu Lys Ala Met Gly Asn Arg Pro Met Glu Met Met
835 840 845

Asp Arg Glu Lys Ala Tyr Ile Pro Glu Leu Gln Ile Ser Phe Met Glu
850 855 860

His Ile Ala Met Pro Ile Tyr Lys Leu Leu Gln Asp Leu Phe Pro Lys
865 870 875 880

Ala Ala Glu Leu Tyr Glu Arg Val Ala Ser Asn Arg Glu His Trp Thr
885 890 895

Lys Val Ser His Lys Phe Thr Ile Arg Gly Leu Pro Ser Asn Asn Ser
900 905 910

Leu Asp Phe Leu Asp Glu Glu Tyr Glu Val Pro Asp Leu Asp Gly Thr
915 920 925

Arg Ala Pro Ile Asn Gly Cys Cys Ser Leu Asp Ala Glu
930 935 940

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

TCRTTNGTNG TNCCYTTCAT RTT

23

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Asn Met Lys Gly Thr Thr Asn Asp
1 5

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1625 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 12..1616

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GAATTCTGAT C ATG GGG TCT AGT GCC ACA GAG ATT GAA GAA TTG GAA AAC	50
Met Gly Ser Ser Ala Thr Glu Ile Glu Glu Leu Glu Asn	
1 5 10	
ACC ACT TTT AAG TAT CTT ACA GGA GAA CAG ACT GAA AAA ATG TGG CAG	98
Thr Thr Phe Lys Tyr Leu Thr Gly Glu Gln Thr Glu Lys Met Trp Gln	
15 20 25	
CGC CTG AAA GGA ATA CTA AGA TGC TTG GTG AAG CAG CTG GAA AGA GGT	146
Arg Leu Lys Gly Ile Leu Arg Cys Leu Val Lys Gln Leu Glu Arg Gly	
30 35 40 45	
GAT GTT AAC GTC GTC GAC TTA AAG AAG AAT ATT GAA TAT GCG GCA TCT	194
Asp Val Asn Val Val Asp Leu Lys Lys Asn Ile Glu Tyr Ala Ala Ser	
50 55 60	

GTG CTG GAA GCA GTT TAT ATC GAT GAA ACA AGA AGA CTT CTG GAT ACT Val Leu Glu Ala Val Tyr Ile Asp Glu Thr Arg Arg Leu Leu Asp Thr 65 70 75	242
GAA GAT GAG CTC AGT GAC ATT CAG ACT GAC TCA GTC CCA TCT GAA GTC Glu Asp Glu Leu Ser Asp Ile Gln Thr Asp Ser Val Pro Ser Glu Val 80 85 90	290
CGG GAC TGG TTG GCT TCT ACC TTT ACA CGG AAA ATG GGG ATG ACA AAA Arg Asp Trp Leu Ala Ser Thr Phe Thr Arg Lys Met Gly Met Thr Lys 95 100 105	338
AAG AAA CCT GAG GAA AAA CCA AAA TTT CGG AGC ATT GTG CAT GCT GTT Lys Lys Pro Glu Glu Lys Pro Lys Phe Arg Ser Ile Val His Ala Val 110 115 120 125	386
CAA GCT GGA ATT TTT GTG GAA AGA ATG TAC CGA AAA ACA TAT CAT ATG Gln Ala Gly Ile Phe Val Glu Arg Met Tyr Arg Lys Thr Tyr His Met 130 135 140	434
GTT GGT TTG GCA TAT CCA GCA GCT GTC ATC GTA ACA TTA AAG GAT GTT Val Gly Leu Ala Tyr Pro Ala Ala Val Ile Val Thr Leu Lys Asp Val 145 150 155	482
GAT AAA TGG TCT TTC GAT GTA TTT GCC CTA AAT GAA GCA AGT GGA GAG Asp Lys Trp Ser Phe Asp Val Phe Ala Leu Asn Glu Ala Ser Gly Glu 160 165 170	530
CAT AGT CTG AAG TTT ATG ATT TAT GAA CTG TTT ACC AGA TAT GAT CTT His Ser Leu Lys Phe Met Ile Tyr Glu Leu Phe Thr Arg Tyr Asp Leu 175 180 185	578
ATC AAC CGT TTC AAG ATT CCT GTT TCT TGC CTA ATC ACC TTT GCA GAA Ile Asn Arg Phe Lys Ile Pro Val Ser Cys Leu Ile Thr Phe Ala Glu 190 195 200 205	626
GCT TTA GAA GTT GGT TAC AGC AAG TAC AAA AAT CCA TAT CAC AAT TTG Ala Leu Glu Val Gly Tyr Ser Lys Tyr Lys Asn Pro Tyr His Asn Leu 210 215 220	674
ATT CAT GCA GCT GAT GTC ACT CAA ACT GTG CAT TAC ATA ATG CTT CAT Ile His Ala Ala Asp Val Thr Gln Thr Val His Tyr Ile Met Leu His 225 230 235	722
ACA GGT ATC ATG CAC TGG CTC ACT GAA CTG GAA ATT TTA GCA ATG GTC Thr Gly Ile Met His Trp Leu Thr Glu Leu Glu Ile Leu Ala Met Val 240 245 250	770
TTT GCT GCT GCC ATT CAT GAT TAT GAG CAT ACA GGG ACA ACA AAC AAC Phe Ala Ala Ala Ile His Asp Tyr Glu His Thr Gly Thr Thr Asn Asn 255 260 265	818
TTT CAC ATT CAG ACA AGG TCA GAT GTT GCC ATT TTG TAT AAT GAT CGC Phe His Ile Gln Thr Arg Ser Asp Val Ala Ile Leu Tyr Asn Asp Arg 270 275 280 285	866
TCT GTC CTT GAG AAT CAC CAC GTG AGT GCA GCT TAT CGA CTT ATG CAA Ser Val Leu Glu Asn His His Val Ser Ala Ala Tyr Arg Leu Met Gln 290 295 300	914
GAA GAA GAA ATG AAT ATC TTG ATA AAT TTA TCC AAA GAT GAC TGG AGG Glu Glu Glu Met Asn Ile Leu Ile Asn Leu Ser Lys Asp Asp Trp Arg 305 310 315	962
GAT CTT CGG AAC CTA GTG ATT GAA ATG GTT TTA TCT ACA GAC ATG TCA Asp Leu Arg Asn Leu Val Ile Glu Met Val Leu Ser Thr Asp Met Ser 320 325 330	1010

GGT CAC TTC CAG CAA ATT AAA AAT ATA AGA AAC AGT TTG CAG CAG CCT Gly His Phe Gln Gln Ile Lys Asn Ile Arg Asn Ser Leu Gln Gln Pro 335 340 345	1058
GAA GGG ATT GAC AGA GCC AAA ACC ATG TCC CTG ATT CTC CAC GCA GCA Glu Gly Ile Asp Arg Ala Lys Thr Met Ser Leu Ile Leu His Ala Ala 350 355 360 365	1106
GAC ATC AGC CAC CCA GCC AAA TCC TGG AAG CTG CAT TAT CGG TGG ACC Asp Ile Ser His Pro Ala Lys Ser Trp Lys Leu His Tyr Arg Trp Thr 370 375 380	1154
ATG GCC CTA ATG GAG GAG TTT TTC CTG CAG GGA GAT AAA GAA GCT GAA Met Ala Leu Met Glu Glu Phe Phe Leu Gln Gly Asp Lys Glu Ala Glu 385 390 395	1202
TTA GGG CTT CCA TTT TCC CCA CTT TGT GAT CGG AAG TCA ACC ATG GTG Leu Gly Leu Pro Phe Ser Pro Leu Cys Asp Arg Lys Ser Thr Met Val 400 405 410	1250
GCC CAG TCA CAA ATA GGT TTC ATC GAT TTC ATA GTA GAG CCA ACA TTT Ala Gln Ser Gln Ile Gly Phe Ile Asp Phe Ile Val Glu Pro Thr Phe 415 420 425	1298
TCT CTT CTG ACA GAC TCA ACA GAG AAA ATT GTT ATT CCT CTT ATA GAG Ser Leu Leu Thr Asp Ser Thr Glu Lys Ile Val Ile Pro Leu Ile Glu 430 435 440 445	1346
GAA GCC TCA AAA GCC GAA ACT TCT TCC TAT GTG GCA AGC AGC TCA ACC Glu Ala Ser Lys Ala Glu Thr Ser Ser Tyr Val Ala Ser Ser Ser Thr 450 455 460	1394
ACC ATT GTG GGG TTA CAC ATT GCT GAT GCA CTA AGA CGA TCA AAT ACA Thr Ile Val Gly Leu His Ile Ala Asp Ala Leu Arg Arg Ser Asn Thr 465 470 475	1442
AAA GGC TCC ATG AGT GAT GGG TCC TAT TCC CCA GAC TAC TCC CTT GCA Lys Gly Ser Met Ser Asp Gly Ser Tyr Ser Pro Asp Tyr Ser Leu Ala 480 485 490	1490
GCA GTG GAC CTG AAG AGT TTC AAG AAC AAC CTG GTG GAC ATC ATT CAG Ala Val Asp Leu Lys Ser Phe Lys Asn Asn Leu Val Asp Ile Ile Gln 495 500 505	1538
CAG AAC AAA GAG AGG TGG AAA GAG TTA GCT GCA CAA GAA GCA AGA ACC Gln Asn Lys Glu Arg Trp Lys Glu Leu Ala Ala Gln Glu Ala Arg Thr 510 515 520 525	1586
AGT TCA CAG AAG TGT GAG TTT ATT CAT CAG TAACTCGAG Ser Ser Gln Lys Cys Glu Phe Ile His Gln 530 535	1625

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 535 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Met	Gly	Ser	Ser	Ala	Thr	Glu	Ile	Glu	Glu	Leu	Glu	Asn	Thr	Thr	Phe
1				5					10					15	

Lys Tyr Leu Thr Gly Glu Gln Thr Glu Lys Met Trp Gln Arg Leu Lys
 20 25 30
 Gly Ile Leu Arg Cys Leu Val Lys Gln Leu Glu Arg Gly Asp Val Asn
 35 40 45
 Val Val Asp Leu Lys Lys Asn Ile Glu Tyr Ala Ala Ser Val Leu Glu
 50 55 60
 Ala Val Tyr Ile Asp Glu Thr Arg Arg Leu Leu Asp Thr Glu Asp Glu
 65 70 75 80
 Leu Ser Asp Ile Gln Thr Asp Ser Val Pro Ser Glu Val Arg Asp Trp
 85 90 95
 Leu Ala Ser Thr Phe Thr Arg Lys Met Gly Met Thr Lys Lys Lys Pro
 100 105 110
 Glu Glu Lys Pro Lys Phe Arg Ser Ile Val His Ala Val Gln Ala Gly
 115 120 125
 Ile Phe Val Glu Arg Met Tyr Arg Lys Thr Tyr His Met Val Gly Leu
 130 135 140
 Ala Tyr Pro Ala Ala Val Ile Val Thr Leu Lys Asp Val Asp Lys Trp
 145 150 155 160
 Ser Phe Asp Val Phe Ala Leu Asn Glu Ala Ser Gly Glu His Ser Leu
 165 170 175
 Lys Phe Met Ile Tyr Glu Leu Phe Thr Arg Tyr Asp Leu Ile Asn Arg
 180 185 190
 Phe Lys Ile Pro Val Ser Cys Leu Ile Thr Phe Ala Glu Ala Leu Glu
 195 200 205
 Val Gly Tyr Ser Lys Tyr Lys Asn Pro Tyr His Asn Leu Ile His Ala
 210 215 220
 Ala Asp Val Thr Gln Thr Val His Tyr Ile Met Leu His Thr Gly Ile
 225 230 235 240
 Met His Trp Leu Thr Glu Leu Glu Ile Leu Ala Met Val Phe Ala Ala
 245 250 255
 Ala Ile His Asp Tyr Glu His Thr Gly Thr Thr Asn Asn Phe His Ile
 260 265 270
 Gln Thr Arg Ser Asp Val Ala Ile Leu Tyr Asn Asp Arg Ser Val Leu
 275 280 285
 Glu Asn His His Val Ser Ala Ala Tyr Arg Leu Met Gln Glu Glu Glu
 290 295 300
 Met Asn Ile Leu Ile Asn Leu Ser Lys Asp Asp Trp Arg Asp Leu Arg
 305 310 315 320
 Asn Leu Val Ile Glu Met Val Leu Ser Thr Asp Met Ser Gly His Phe
 325 330 335
 Gln Gln Ile Lys Asn Ile Arg Asn Ser Leu Gln Gln Pro Glu Gly Ile
 340 345 350
 Asp Arg Ala Lys Thr Met Ser Leu Ile Leu His Ala Ala Asp Ile Ser
 355 360 365

His Pro Ala Lys Ser Trp Lys Leu His Tyr Arg Trp Thr Met Ala Leu
 370 375 380

Met Glu Glu Phe Phe Leu Gln Gly Asp Lys Glu Ala Glu Leu Gly Leu
 385 390 395 400

Pro Phe Ser Pro Leu Cys Asp Arg Lys Ser Thr Met Val Ala Gln Ser
 405 410 415

Gln Ile Gly Phe Ile Asp Phe Ile Val Glu Pro Thr Phe Ser Leu Leu
 420 425 430

Thr Asp Ser Thr Glu Lys Ile Val Ile Pro Leu Ile Glu Glu Ala Ser
 435 440 445

Lys Ala Glu Thr Ser Ser Tyr Val Ala Ser Ser Ser Thr Thr Ile Val
 450 455 460

Gly Leu His Ile Ala Asp Ala Leu Arg Arg Ser Asn Thr Lys Gly Ser
 465 470 475 480

Met Ser Asp Gly Ser Tyr Ser Pro Asp Tyr Ser Leu Ala Ala Val Asp
 485 490 495

Leu Lys Ser Phe Lys Asn Asn Leu Val Asp Ile Ile Gln Gln Asn Lys
 500 505 510

Glu Arg Trp Lys Glu Leu Ala Ala Gln Glu Ala Arg Thr Ser Ser Gln
 515 520 525

Lys Cys Glu Phe Ile His Gln
 530 535

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2693 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 176..2077

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GTCGCTTCAA TATTTCAAAA TGGATCCGGT TCTGTGGCGG GTGCGAGAGT GAGGCTGTGG 60

GGGACCTCCA GGCCGAACCT CCGCGAAGCC TCGGCCTTCT GCGTGCCCTG GCCCCGGGAG 120

GATAAGGATT TCCCTTCCCT CCTACTTGCG CGCGGAGCCG AGCTCTTGTT GAGCT ATG 178
 Met
 1

GAG TCG CCA ACC AAG GAG ATT GAA GAA TTT GAG AGC AAC TCT CTG AAA 226
 Glu Ser Pro Thr Lys Glu Ile Glu Glu Phe Glu Ser Asn Ser Leu Lys
 5 10 15

TAC CTG CAA CCG GAA CAG ATC GAG AAA ATC TGG CTT CGG CTC CGC GGG 274
 Tyr Leu Gln Pro Glu Gln Ile Glu Lys Ile Trp Leu Arg Leu Arg Gly
 20 25 30

CTG AGG AAA TAT AAG AAA ACG TCC CAG AGA TTA CGG TCT TTG GTC AAA Leu Arg Lys Tyr Lys Lys Thr Ser Gln Arg Leu Arg Ser Leu Val Lys 35 40 45	322
CAA TTA GAG AGA GGG GAA GCT TCA GTG GTA GAT CTT AAG AAG AAT TTG Gln Leu Glu Arg Gly Glu Ala Ser Val Val Asp Leu Lys Lys Asn Leu 50 55 60 65	370
GAA TAT GCA GCC ACA GTG CTT GAA TCT GTG TAT ATT GAT GAA ACA AGG Glu Tyr Ala Ala Thr Val Leu Glu Ser Val Tyr Ile Asp Glu Thr Arg 70 75 80	418
AGA CTC CTG GAT ACA GAG GAT GAG CTC AGT GAC ATT CAG TCA GAT GCT Arg Leu Leu Asp Thr Glu Asp Glu Leu Ser Asp Ile Gln Ser Asp Ala 85 90 95	466
GTG CCT TCT GAG GTC CGA GAC TGG CTG GCC TCC ACC TTC ACG CGG CAG Val Pro Ser Glu Val Arg Asp Trp Leu Ala Ser Thr Phe Thr Arg Gln 100 105 110	514
ATG GGG ATG ATG CTC AGG AGG AGC GAC GAG AAG CCC CGG TTC AAG AGC Met Gly Ser Met Met Leu Arg Arg Ser Asp Glu Lys Pro Arg Phe Lys Ser 115 120 125	562
ATC GTT CAC GCA GTG CAG GCT GGG ATA TTT GTG GAG AGA ATG TAT AGA Ile Val His Ala Val Gln Ala Gly Ile Phe Val Glu Arg Met Tyr Arg 130 135 140 145	610
CGG ACA TCA AAC ATG GTT GGA CTG AGC TAT CCA CCA GCT GTT ATT GAG Arg Thr Ser Asn Met Val Gly Leu Ser Tyr Pro Pro Ala Val Ile Glu 150 155 160	658
GCA TTA AAG GAT GTG GAC AAG TGG TCC TTT GAC GTC TTT TCC CTC AAT Ala Leu Lys Asp Val Asp Lys Trp Ser Phe Asp Val Phe Ser Leu Asn 165 170 175	706
GAG GCC AGT GGG GAT CAT GCA CTG AAA TTT ATT TTC TAT GAA CTA CTC Glu Ala Ser Gly Asp His Ala Leu Lys Phe Ile Phe Tyr Glu Leu Leu 180 185 190	754
ACA CGT TAT GAT CTG ATC AGC CGT TTC AAG ATC CCC ATT TCT GCA CTT Thr Arg Tyr Asp Leu Ile Ser Arg Phe Lys Ile Pro Ile Ser Ala Leu 195 200 205	802
GTC TCA TTT GTG GAG GCC CTG GAA GTG GGA TAC AGC AAG CAC AAA AAT Val Ser Phe Val Glu Ala Leu Glu Val Gly Tyr Ser Lys His Lys Asn 210 215 220 225	850
CCT TAC CAT AAC TTA ATG CAC GCT GCC GAT GTT ACA CAG ACA GTG CAT Pro Tyr His Asn Leu Met His Ala Ala Asp Val Thr Gln Thr Val His 230 235 240	898
TAC CTC CTC TAT AAG ACA GGA GTG GCG AAC TGG CTG ACG GAG CTG GAG Tyr Leu Leu Tyr Lys Thr Gly Val Ala Asn Trp Leu Thr Glu Leu Glu 245 250 255	946
ATC TTT GCT ATA ATC TTC TCA GCT GCC ATC CAT GAC TAC GAG CAT ACC Ile Phe Ala Ile Ile Phe Ser Ala Ala Ile His Asp Tyr Glu His Thr 260 265 270	994
GGA ACC ACC AAC AAT TTC CAC ATT CAG ACT CGG TCT GAT CCA GCT ATT Gly Thr Thr Asn Asn Phe His Ile Gln Thr Arg Ser Asp Pro Ala Ile 275 280 285	1042
CTG TAT AAT GAC AGA TCT GTA CTG GAG AAT CAC CAT TTA AGT GCA GCT Leu Tyr Asn Asp Arg Ser Val Leu Glu Asn His His Leu Ser Ala Ala 290 295 300 305	1090

TAT CGC CTT CTG CAA GAT GAC GAG GAA ATG AAT ATT TTG ATT AAC CTC Tyr Arg Leu Leu Gln Asp Asp Glu Glu Met Asn Ile Leu Ile Asn Leu 310 315 320	1138
TCA AAG GAT GAC TGG AGG GAG TTT CGA ACC TTG GTA ATT GAA ATG GTG Ser Lys Asp Asp Trp Arg Glu Phe Arg Thr Leu Val Ile Glu Met Val 325 330 335	1186
ATG GCC ACA GAT ATG TCT TGT CAC TTC CAA CAA ATC AAA GCA ATG AAG Met Ala Thr Asp Met Ser Cys His Phe Gln Gln Ile Lys Ala Met Lys 340 345 350	1234
ACT GCT CTG CAG CAG CCA GAA GCC ATT GAA AAG CCA AAA GCC TTA TCC Thr Ala Leu Gln Gln Pro Glu Ala Ile Glu Lys Pro Lys Ala Leu Ser 355 360 365	1282
CTT ATG CTG CAT ACA GCA GAT ATT AGC CAT CCA GCA AAA GCA TGG GAC Leu Met Leu His Thr Ala Asp Ile Ser His Ala Lys Ala Trp Asp 370 375 380 385	1330
CTC CAT CAT CGC TGG ACA ATG TCA CTC CTG GAG GAG TTC TTC AGA CAG Leu His His Arg Trp Thr Met Ser Leu Leu Glu Glu Phe Phe Arg Gln 390 395 400	1378
GGT GAC AGA GAA GCA GAG CTG GGG CTG CCT TTT TCT CCT CTG TGT GAC Gly Asp Arg Glu Ala Glu Leu Gly Leu Pro Phe Ser Pro Leu Cys Asp 405 410 415	1426
CGA AAG TCC ACT ATG GTT GCT CAG TCA CAA GTA GGT TTC ATT GAT TTC Arg Lys Ser Thr Met Val Ala Gln Ser Gln Val Gly Phe Ile Asp Phe 420 425 430	1474
ATC GTG GAA CCC ACC TTC ACT GTG CTT ACG GAC ATG ACC GAG AAG ATT Ile Val Glu Pro Thr Phe Thr Val Leu Thr Asp Met Thr Glu Lys Ile 435 440 445	1522
GTG AGT CCA TTA ATC GAT GAA ACC TCT CAA ACT GGT GGG ACA GGA CAG Val Ser Pro Leu Ile Asp Glu Thr Ser Gln Thr Gly Gly Thr Gly Gln 450 455 460 465	1570
AGG CGT TCG AGT TTG AAT AGC ATC AGC TCG TCA GAT GCC AAG CGA TCA Arg Arg Ser Ser Leu Asn Ser Ile Ser Ser Ser Asp Ala Lys Arg Ser 470 475 480	1618
GGT GTC AAG ACC TCT GGT TCA GAG GGA AGT GCC CCG ATC AAC AAT TCT Gly Val Lys Thr Ser Gly Ser Glu Gly Ser Ala Pro Ile Asn Asn Ser 485 490 495	1666
GTC ATC TCC GTT GAC TAT AAG AGC TTT AAA GCT ACT TGG ACG GAA GTG Val Ile Ser Val Asp Tyr Lys Ser Phe Lys Ala Thr Trp Thr Glu Val 500 505 510	1714
GTG CAC ATC AAT CGG GAG AGA TGG AGG GCC AAG GTA CCC AAA GAG GAG Val His Ile Asn Arg Glu Arg Trp Arg Ala Lys Val Pro Lys Glu Glu 515 520 525	1762
AAG GCC AAG AAG GAA GCA GAG GAA AAG GCT CGC CTG GCC GCA GAG GAG Lys Ala Lys Lys Glu Ala Glu Glu Lys Ala Arg Leu Ala Ala Glu Glu 530 535 540 545	1810
CAG CAA AAG GAA ATG GAA GCC AAA AGC CAG GCT GAA GAA GGC GCA TCT Gln Gln Lys Glu Met Glu Ala Lys Ser Gln Ala Glu Glu Gly Ala Ser 550 555 560	1858
GGC AAA GCT GAG AAA AAG ACG TCT GGA GAA ACT AAG AAT CAA GTC AAT Gly Lys Ala Glu Lys Lys Thr Ser Gly Glu Thr Lys Asn Gln Val Asn 565 570 575	1906

GGA ACA CGG GCA AAC AAA AGT GAC AAC CCT CGT GGG AAA AAT TCC AAA Gly Thr Arg Ala Asn Lys Ser Asp Asn Pro Arg Gly Lys Asn Ser Lys 580 585 590	1954
GCC GAG AAG TCA TCA GGA GAA CAG CAA CAG AAT GGT GAC TTC AAA GAT Ala Glu Lys Ser Ser Gly Glu Gln Gln Gln Asn Gly Asp Phe Lys Asp 595 600 605	2002
GGT AAA AAT AAG ACA GAC AAG AAG GAT CAC TCT AAC ATC GGA AAT GAT Gly Lys Asn Lys Thr Asp Lys Lys Asp His Ser Asn Ile Gly Asn Asp 610 615 620 625	2050
TCA AAG AAA ACA GAT GAT TCA CAA GAG TAAAAAAGAC CTCATAGACA Ser Lys Lys Thr Asp Asp Ser Gln Glu 630	2097
ATAAAAGAGG CTGCCAGTGT CTTGCATCAT TCTAGCTGAG CTTCTTCATT CTCCTTCTTC	2157
TCCTTCTTCC ACAAGACCCC ATATCTGGAG AAGGTGTACA ACTTTCAAAC ACAAGCCCCC	2217
CACCCCTGA CCCTTGGCCT TCCCTCACAC CATCTCCTTC CAGGGGATGA ATCTTTGGGG	2277
GTTGGTTTGA GGTCTTAGAA CTCTGGGGGA TATTCCTCTG AGCAAAACAA ACAACGTGAG	2337
ATTTTACTC AAACAGAAAC AAAACATGAA GGGGCATCCT CAAAATCCTT TGCTAATGAC	2397
CTGGCTTTCA AGGCATCTGT CTGGCCTGAT GAGAATGGAC ATCCTGGATA TGCTGGGAGA	2457
GGCCTGAAAA AAGCCACACA CACAGTAATT GCCATTTTAT GACTGTCAAT GCCGTTACTT	2517
TAAATGTTGT CATTTTTGCA CTGGCTACTG ATGATACAGC CATGCTGACA TTCATCACCG	2577
CAAAGATGAT GATTCCAGTC TCTGGTTCCT TTCCTGAGTC AGGAACATTT GTTTTCTCCA	2637
ATTCCTTTC AGACTTAAAA TTGTTCTTAT GCTTTTTTTC CCACTTCTGT AATACA	2693

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 634 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Met	Glu	Ser	Pro	Thr	Lys	Glu	Ile	Glu	Glu	Phe	Glu	Ser	Asn	Ser	Leu	1	5	10	15
Lys	Tyr	Leu	Gln	Pro	Glu	Gln	Ile	Glu	Lys	Ile	Trp	Leu	Arg	Leu	Arg	20	25	30	
Gly	Leu	Arg	Lys	Tyr	Lys	Lys	Thr	Ser	Gln	Arg	Leu	Arg	Ser	Leu	Val	35	40	45	
Lys	Gln	Leu	Glu	Arg	Gly	Glu	Ala	Ser	Val	Val	Asp	Leu	Lys	Lys	Asn	50	55	60	
Leu	Glu	Tyr	Ala	Ala	Thr	Val	Leu	Glu	Ser	Val	Tyr	Ile	Asp	Glu	Thr	65	70	75	80
Arg	Arg	Leu	Leu	Asp	Thr	Glu	Asp	Glu	Leu	Ser	Asp	Ile	Gln	Ser	Asp	85	90	95	

Ala Val Pro Ser Glu Val Arg Asp Trp Leu Ala Ser Thr Phe Thr Arg
100 110
Gln Met Gly Met Met Leu Arg Arg Ser Asp Glu Lys Pro Arg Phe Lys
115 120 125
Ser Ile Val His Ala Val Gln Ala Gly Ile Phe Val Glu Arg Met Tyr
130 135 140
Arg Arg Thr Ser Asn Met Val Gly Leu Ser Tyr Pro Pro Ala Val Ile
145 150 155 160
Glu Ala Leu Lys Asp Val Asp Lys Trp Ser Phe Asp Val Phe Ser Leu
165 170 175
Asn Glu Ala Ser Gly Asp His Ala Leu Lys Phe Ile Phe Tyr Glu Leu
180 185 190
Leu Thr Arg Tyr Asp Leu Ile Ser Arg Phe Lys Ile Pro Ile Ser Ala
195 200 205
Leu Val Ser Phe Val Glu Ala Leu Glu Val Gly Tyr Ser Lys His Lys
210 215 220
Asn Pro Tyr His Asn Leu Met His Ala Ala Asp Val Thr Gln Thr Val
225 230 235 240
His Tyr Leu Leu Tyr Lys Thr Gly Val Ala Asn Trp Leu Thr Glu Leu
245 250 255
Glu Ile Phe Ala Ile Ile Phe Ser Ala Ala Ile His Asp Tyr Glu His
260 265 270
Thr Gly Thr Thr Asn Asn Phe His Ile Gln Thr Arg Ser Asp Pro Ala
275 280 285
Ile Leu Tyr Asn Asp Arg Ser Val Leu Glu Asn His His Leu Ser Ala
290 295 300
Ala Tyr Arg Leu Leu Gln Asp Asp Glu Glu Met Asn Ile Leu Ile Asn
305 310 315 320
Leu Ser Lys Asp Asp Trp Arg Glu Phe Arg Thr Leu Val Ile Glu Met
325 330 335
Val Met Ala Thr Asp Met Ser Cys His Phe Gln Gln Ile Lys Ala Met
340 345 350
Lys Thr Ala Leu Gln Gln Pro Glu Ala Ile Glu Lys Pro Lys Ala Leu
355 360 365
Ser Leu Met Leu His Thr Ala Asp Ile Ser His Pro Ala Lys Ala Trp
370 375 380
Asp Leu His His Arg Trp Thr Met Ser Leu Leu Glu Glu Phe Phe Arg
385 390 395 400
Gln Gly Asp Arg Glu Ala Glu Leu Gly Leu Pro Phe Ser Pro Leu Cys
405 410 415
Asp Arg Lys Ser Thr Met Val Ala Gln Ser Gln Val Gly Phe Ile Asp
420 425 430
Phe Ile Val Glu Pro Thr Phe Thr Val Leu Thr Asp Met Thr Glu Lys
435 440 445

Ile Val Ser Pro Leu Ile Asp Glu Thr Ser Gln Thr Gly Gly Thr Gly
 450 455 460
 Gln Arg Arg Ser Ser Leu Asn Ser Ile Ser Ser Ser Asp Ala Lys Arg
 465 470 475 480
 Ser Gly Val Lys Thr Ser Gly Ser Glu Gly Ser Ala Pro Ile Asn Asn
 485 490 495
 Ser Val Ile Ser Val Asp Tyr Lys Ser Phe Lys Ala Thr Trp Thr Glu
 500 505 510
 Val Val His Ile Asn Arg Glu Arg Trp Arg Ala Lys Val Pro Lys Glu
 515 520 525
 Glu Lys Ala Lys Lys Glu Ala Glu Glu Lys Ala Arg Leu Ala Ala Glu
 530 535 540
 Glu Gln Gln Lys Glu Met Glu Ala Lys Ser Gln Ala Glu Glu Gly Ala
 545 550 555 560
 Ser Gly Lys Ala Glu Lys Lys Thr Ser Gly Glu Thr Lys Asn Gln Val
 565 570 575
 Asn Gly Thr Arg Ala Asn Lys Ser Asp Asn Pro Arg Gly Lys Asn Ser
 580 585 590
 Lys Ala Glu Lys Ser Ser Gly Glu Gln Gln Gln Asn Gly Asp Phe Lys
 595 600 605
 Asp Gly Lys Asn Lys Thr Asp Lys Lys Asp His Ser Asn Ile Gly Asn
 610 615 620
 Asp Ser Lys Lys Thr Asp Asp Ser Gln Glu
 625 630

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2077 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 2..1693

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

A CCG ACA TCA AAC ATG GTT GGA CTG AGC TAT CCA CCA GCT GTT ATT	46
Arg Thr Ser Asn Met Val Gly Leu Ser Tyr Pro Pro Ala Val Ile	
1 5 10 15	
GAG GCA TTA AAG GAT GTG GAC AAG TGG TCC TTT GAC GTC TTT TCC CTC	94
Glu Ala Leu Lys Asp Val Asp Lys Trp Ser Phe Asp Val Phe Ser Leu	
20 25 30	
AAT GAG GCC AGT GGG GAT CAT GCA CTG AAA TTT ATT TTC TAT GAA CTA	142
Asn Glu Ala Ser Gly Asp His Ala Leu Lys Phe Ile Phe Tyr Glu Leu	
35 40 45	

CTC	ACA	CGT	TAT	GAT	CTG	ATC	AGC	CGT	TTC	AAG	ATC	CCC	ATT	TCT	GCA	190
Leu	Thr	Arg	Tyr	Asp	Leu	Ile	Ser	Arg	Phe	Lys	Ile	Pro	Ile	Ser	Ala	
		50					55					60				
CTT	GTC	TCA	TTT	GTG	GAG	GCC	CTG	GAA	GTG	GGA	TAC	AGC	AAG	CAC	AAA	238
Leu	Val	Ser	Phe	Val	Glu	Ala	Leu	Glu	Val	Gly	Tyr	Ser	Lys	His	Lys	
		65				70					75					
AAT	CCT	TAC	CAT	AAC	TTA	ATG	CAC	GCT	GCC	GAT	GTT	ACA	CAG	ACA	GTG	286
Asn	Pro	Tyr	His	Asn	Leu	Met	His	Ala	Ala	Asp	Val	Thr	Gln	Thr	Val	
		80			85					90					95	
CAT	TAC	CTC	CTC	TAT	AAG	ACA	GGA	GTG	GCG	AAC	TGG	CTG	ACG	GAG	CTG	334
His	Tyr	Leu	Leu	Tyr	Lys	Thr	Gly	Val	Ala	Asn	Trp	Leu	Thr	Glu	Leu	
				100					105					110		
GAG	ATC	TTT	GCT	ATA	ATC	TTC	TCA	GCT	GCC	ATC	CAT	GAC	TAC	GAG	CAT	382
Glu	Ile	Phe	Ala	Ile	Ile	Phe	Ser	Ala	Ala	Ile	His	Asp	Tyr	Glu	His	
			115					120					125			
ACC	GGA	ACC	ACC	AAC	AAT	TTC	CAC	ATT	CAG	ACT	CGG	TCT	GAT	CCA	GCT	430
Thr	Gly	Thr	Thr	Asn	Asn	Phe	His	Ile	Gln	Thr	Arg	Ser	Asp	Pro	Ala	
		130					135					140				
ATT	CTG	TAT	AAT	GAC	AGA	TCT	GTA	CTG	GAG	AAT	CAC	CAT	TTA	AGT	GCA	478
Ile	Leu	Tyr	Asn	Asp	Arg	Ser	Val	Leu	Glu	Asn	His	His	Leu	Ser	Ala	
		145				150					155					
GCT	TAT	CGC	CTT	CTG	CAA	GAT	GAC	GAG	GAA	ATG	AAT	ATT	TTG	ATT	AAC	526
Ala	Tyr	Arg	Leu	Leu	Gln	Asp	Asp	Glu	Glu	Met	Asn	Ile	Leu	Ile	Asn	
					165					170					175	
CTC	TCA	AAG	GAT	GAC	TGG	AGG	GAG	TTT	CGA	ACC	TTG	GTA	ATT	GAA	ATG	574
Leu	Ser	Lys	Asp	Asp	Trp	Arg	Glu	Phe	Arg	Thr	Leu	Val	Ile	Glu	Met	
				180					185					190		
GTG	ATG	GCC	ACA	GAT	ATG	TCT	TGT	CAC	TTC	CAA	CAA	ATC	AAA	GCA	ATG	622
Val	Met	Ala	Thr	Asp	Met	Ser	Cys	His	Phe	Gln	Gln	Ile	Lys	Ala	Met	
			195					200					205			
AAG	ACT	GCT	CTG	CAG	CAG	CCA	GAA	GCC	ATT	GAA	AAG	CCA	AAA	GCC	TTA	670
Lys	Thr	Ala	Leu	Gln	Gln	Pro	Glu	Ala	Ile	Glu	Lys	Pro	Lys	Ala	Leu	
		210					215					220				
TCC	CTT	ATG	CTG	CAT	ACA	GCA	GAT	ATT	AGC	CAT	CCA	GCA	AAA	GCA	TGG	718
Ser	Leu	Met	Leu	His	Thr	Ala	Asp	Ile	Ser	His	Pro	Ala	Lys	Ala	Trp	
		225				230					235					
GAC	CTC	CAT	CAT	CGC	TGG	ACA	ATG	TCA	CTC	CTG	GAG	GAG	TTC	TTC	AGA	766
Asp	Leu	His	His	Arg	Trp	Thr	Met	Ser	Leu	Leu	Glu	Glu	Phe	Phe	Arg	
				245						250					255	
CAG	GGT	GAC	AGA	GAA	GCA	GAG	CTG	GGG	CTG	CCT	TTT	TCT	CCT	CTG	TGT	814
Gln	Gly	Asp	Arg	Glu	Ala	Glu	Leu	Gly	Leu	Pro	Phe	Ser	Pro	Leu	Cys	
				260					265					270		
GAC	CGA	AAG	TCC	ACT	ATG	GTT	GCT	CAG	TCA	CAA	GTA	GGT	TTC	ATT	GAT	862
Asp	Arg	Lys	Ser	Thr	Met	Val	Ala	Gln	Ser	Gln	Val	Gly	Phe	Ile	Asp	
			275					280					285			
TTC	ATC	GTG	GAA	CCC	ACC	TTC	ACT	GTG	CTT	ACG	GAC	ATG	ACC	GAG	AAG	910
Phe	Ile	Val	Glu	Pro	Thr	Phe	Thr	Val	Leu	Thr	Asp	Met	Thr	Glu	Lys	
		290					295					300				
ATT	GTG	AGT	CCA	TTA	ATC	GAT	GAA	ACC	TCT	CAA	ACT	GGT	GGG	ACA	GGA	958
Ile	Val	Ser	Pro	Leu	Ile	Asp	Glu	Thr	Ser	Gln	Thr	Gly	Gly	Thr	Gly	
		305				310					315					

CAG AGG CGT TCG AGT TTG AAT AGC ATC AGC TCG TCA GAT GCC AAG CGA Gln Arg Arg Ser Ser Leu Asn Ser Ile Ser Ser Ser Asp Ala Lys Arg 320 325 330 335	1006
TCA GGT GTC AAG ACC TCT GGT TCA GAG GGA AGT GCC CCG ATC AAC AAT Ser Gly Val Lys Thr Ser Gly Ser Glu Gly Ser Ala Pro Ile Asn Asn 340 345 350	1054
TCT GTC ATC TCC GTT GAC TAT AAG AGC TTT AAA GCT ACT TGG ACG GAA Ser Val Ile Ser Val Asp Tyr Lys Ser Phe Lys Ala Thr Trp Thr Glu 355 360 365	1102
GTG GTG CAC ATC AAT CGG GAG AGA TGG AGG GCC AAG GTA CCC AAA GAG Val Val His Ile Asn Arg Glu Arg Trp Arg Ala Lys Val Pro Lys Glu 370 375 380	1150
GAG AAG GCC AAG AAG GAA GCA GAG GAA AAG GCT CGC CTG GCC GCA GAG Glu Lys Ala Lys Lys Glu Ala Glu Glu Lys Ala Arg Leu Ala Ala Glu 385 390 395	1198
GAG CAG CAA AAG GAA ATG GAA GCC AAA AGC CAG GCT GAA GAA GGC GCA Glu Gln Gln Lys Glu Met Glu Ala Lys Ser Gln Ala Glu Glu Gly Ala 400 405 410 415	1246
TCT GGC AAA GCT GAG AAA AAG ACG TCT GGA GAA ACT AAG AAT CAA GTC Ser Gly Lys Ala Glu Lys Lys Thr Ser Gly Glu Thr Lys Asn Gln Val 420 425 430	1294
AAT GGA ACA CGG GCA AAC AAA AGT GAC AAC CCT CGT GGG AAA AAT TCC Asn Gly Thr Arg Ala Asn Lys Ser Asp Asn Pro Arg Gly Lys Asn Ser 435 440 445	1342
AAA GCT GAG AAG TCA TCA GGA GAA CAG CAA CAG AAT GGT GAC TTC AAA Lys Ala Glu Lys Ser Ser Gly Glu Gln Gln Gln Asn Gly Asp Phe Lys 450 455 460	1390
GAT GGT AAA AAT AAG ACA GAC AAG AAG GAT CAC TCT AAC ATC GGA AAT Asp Gly Lys Asn Lys Thr Asp Lys Lys Asp His Ser Asn Ile Gly Asn 465 470 475	1438
GAT TCA AAG AAA ACA GAT GGC ACA AAA CAG CGT TCT CAC GGC TCA CCA Asp Ser Lys Lys Thr Asp Gly Thr Lys Gln Arg Ser His Gly Ser Pro 480 485 490 495	1486
GCC CCA AGC ACC AGC TCC ACG TGT CGC CTT ACG TTG CCA GTC ATC AAG Ala Pro Ser Thr Ser Ser Thr Cys Arg Leu Thr Leu Pro Val Ile Lys 500 505 510	1534
CCT CCT TTG CGT CAT TTT AAA CGC CCT GCT TAC GCA TCT AGC TCC TAT Pro Pro Leu Arg His Phe Lys Arg Pro Ala Tyr Ala Ser Ser Ser Tyr 515 520 525	1582
GCA CCT TCA GTC TCA AAG AAA ACT GAT GAG CAT CCT GCA AGG TAC AAG Ala Pro Ser Val Ser Lys Lys Thr Asp Glu His Pro Ala Arg Tyr Lys 530 535 540	1630
ATG CTA GAT CAG AGG ATC AAA ATG AAA AAG ATT CAG AAC ATC TCA CAT Met Leu Asp Gln Arg Ile Lys Met Lys Lys Ile Gln Asn Ile Ser His 545 550 555	1678
AAC TGG AAC AGA AAA TAGGCCGAGG GGAAGAAGAG AGGGAGTGAA GGAGGGTCTA Asn Trp Asn Arg Lys 560	1733
CCTATCTGCT TCTCAGCACC CACTGGCCAC AGCAGGACAC ACCTCCAAGA CCCTTGGAGG	1793
CTGTTGGAGC AGGTACTATC CTGGTTGACT CCACCAAGGT GAAATGAAAG TTGTATGTGA	1853

TTTTCTCTT TGTTGTTCTT GTATAGACTT TTCAATTGCT GTATGTGGGA TCAGCCCAGA	1913
CGCCAGCAAC AAAGTAGCAA GAGGGGTGTT TTTATGGTAT AAGTCTCTAA AAGTCTAAAT	1973
TGGACCAAAA TTTAAATGAC ACAAAGTTAA AAAAAATAA AATTCCTCTC ATTGCCACTT	2033
TTTTCAATCT CTAAAAGTTA CTTGCCCCCA AAAGAATATT GGTC	2077

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 564 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Arg	Thr	Ser	Asn	Met	Val	Gly	Leu	Ser	Tyr	Pro	Pro	Ala	Val	Ile	Glu	1	5	10	15
Ala	Leu	Lys	Asp	Val	Asp	Lys	Trp	Ser	Phe	Asp	Val	Phe	Ser	Leu	Asn	20	25	30	
Glu	Ala	Ser	Gly	Asp	His	Ala	Leu	Lys	Phe	Ile	Phe	Tyr	Glu	Leu	Leu	35	40	45	
Thr	Arg	Tyr	Asp	Leu	Ile	Ser	Arg	Phe	Lys	Ile	Pro	Ile	Ser	Ala	Leu	50	55	60	
Val	Ser	Phe	Val	Glu	Ala	Leu	Glu	Val	Gly	Tyr	Ser	Lys	His	Lys	Asn	65	70	75	80
Pro	Tyr	His	Asn	Leu	Met	His	Ala	Ala	Asp	Val	Thr	Gln	Thr	Val	His	85	90	95	
Tyr	Leu	Leu	Tyr	Lys	Thr	Gly	Val	Ala	Asn	Trp	Leu	Thr	Glu	Leu	Glu	100	105	110	
Ile	Phe	Ala	Ile	Ile	Phe	Ser	Ala	Ala	Ile	His	Asp	Tyr	Glu	His	Thr	115	120	125	
Gly	Thr	Thr	Asn	Asn	Phe	His	Ile	Gln	Thr	Arg	Ser	Asp	Pro	Ala	Ile	130	135	140	
Leu	Tyr	Asn	Asp	Arg	Ser	Val	Leu	Glu	Asn	His	His	Leu	Ser	Ala	Ala	145	150	155	160
Tyr	Arg	Leu	Leu	Gln	Asp	Asp	Glu	Glu	Met	Asn	Ile	Leu	Ile	Asn	Leu	165	170	175	
Ser	Lys	Asp	Asp	Trp	Arg	Glu	Phe	Arg	Thr	Leu	Val	Ile	Glu	Met	Val	180	185	190	
Met	Ala	Thr	Asp	Met	Ser	Cys	His	Phe	Gln	Gln	Ile	Lys	Ala	Met	Lys	195	200	205	
Thr	Ala	Leu	Gln	Gln	Pro	Glu	Ala	Ile	Glu	Lys	Pro	Lys	Ala	Leu	Ser	210	215	220	
Leu	Met	Leu	His	Thr	Ala	Asp	Ile	Ser	His	Pro	Ala	Lys	Ala	Trp	Asp	225	230	235	240
Leu	His	His	Arg	Trp	Thr	Met	Ser	Leu	Leu	Glu	Glu	Phe	Phe	Arg	Gln	245	250	255	

Gly Asp Arg Glu Ala Glu Leu Gly Leu Pro Phe Ser Pro Leu Cys Asp
260 265 270
Arg Lys Ser Thr Met Val Ala Gln Ser Gln Val Gly Phe Ile Asp Phe
275 280 285
Ile Val Glu Pro Thr Phe Thr Val Leu Thr Asp Met Thr Glu Lys Ile
290 295 300
Val Ser Pro Leu Ile Asp Glu Thr Ser Gln Thr Gly Gly Thr Gly Gln
305 310 315 320
Arg Arg Ser Ser Leu Asn Ser Ile Ser Ser Ser Asp Ala Lys Arg Ser
325 330 335
Gly Val Lys Thr Ser Gly Ser Glu Gly Ser Ala Pro Ile Asn Asn Ser
340 345 350
Val Ile Ser Val Asp Tyr Lys Ser Phe Lys Ala Thr Trp Thr Glu Val
355 360 365
Val His Ile Asn Arg Glu Arg Trp Arg Ala Lys Val Pro Lys Glu Glu
370 375 380
Lys Ala Lys Lys Glu Ala Glu Glu Lys Ala Arg Leu Ala Ala Glu Glu
385 390 395 400
Gln Gln Lys Glu Met Glu Ala Lys Ser Gln Ala Glu Glu Gly Ala Ser
405 410 415
Gly Lys Ala Glu Lys Lys Thr Ser Gly Glu Thr Lys Asn Gln Val Asn
420 425 430
Gly Thr Arg Ala Asn Lys Ser Asp Asn Pro Arg Gly Lys Asn Ser Lys
435 440 445
Ala Glu Lys Ser Ser Gly Glu Gln Gln Gln Asn Gly Asp Phe Lys Asp
450 455 460
Gly Lys Asn Lys Thr Asp Lys Lys Asp His Ser Asn Ile Gly Asn Asp
465 470 475 480
Ser Lys Lys Thr Asp Gly Thr Lys Gln Arg Ser His Gly Ser Pro Ala
485 490 495
Pro Ser Thr Ser Ser Thr Cys Arg Leu Thr Leu Pro Val Ile Lys Pro
500 505 510
Pro Leu Arg His Phe Lys Arg Pro Ala Tyr Ala Ser Ser Ser Tyr Ala
515 520 525
Pro Ser Val Ser Lys Lys Thr Asp Glu His Pro Ala Arg Tyr Lys Met
530 535 540
Leu Asp Gln Arg Ile Lys Met Lys Lys Ile Gln Asn Ile Ser His Asn
545 550 555 560
Trp Asn Arg Lys

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

TACGAAGCTT TGATGGGGTC TACTGCTAC

29

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

TACGAAGCTT TGATGGTTGG CTTGGCATAT C

31

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

ATTACCCCTC ATAAAG

16

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

TACGAAGCTT TGATGCGCCG ACAGCCTGC

29

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 bas pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GGTCTCCTGT TGCAGATATT G